

- Alignment Length 37
- Location of Alignment in SEQ ID NO 1095: from 1 to 34
- Alignment No. 9102
- gi No. 2501189
- % Identity 97.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1095: from 1 to 34
- Alignment No. 9103
- gi No. 2582665
- % Identity 92.3
- Alignment Length 39
- Location of Alignment in SEQ ID NO 1095: from 1 to 36
- Alignment No. 9104
- gi No. 3650384
- % Identity 71.9
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1095: from 1 to 31

Maximum Length Sequence corresponding to clone ID 246878

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1096
- Ceres seq_id 1499627

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1097
- Ceres seq_id 1499628
- Location of start within SEQ ID NO 1096: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9105
- gi No. 4006881
- % Identity 78.9
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1097: from 8 to 45

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1098
- Ceres seq_id 1499629
- Location of start within SEQ ID NO 1096: at 331 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1099
- Ceres seq_id 1499630
- Location of start within SEQ ID NO 1096: at 337 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 247172

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1100
- Ceres seq_id 1499649

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1101
- Ceres seq_id 1499650
- Location of start within SEQ ID NO 1100: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9106
- 11-S plant seed storage protein
- Location within SEQ ID NO 1101: from 18 to 105 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1102
- Ceres seq_id 1499651
- Location of start within SEQ ID NO 1100: at 58 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1103
- Ceres seq_id 1499652
- Location of start within SEQ ID NO 1100: at 94 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 247194

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1104
- Ceres seq_id 1499655

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1105
- Ceres seq_id 1499656
- Location of start within SEQ ID NO 1104: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9107
- gi No. 1071974
- % Identity 72.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1105: from 26 to 65
- Alignment No. 9108
- gi No. 1173217
- % Identity 72.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1105: from 26 to 65
- Alignment No. 9109
- gi No. 1173218
- % Identity 95
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1105: from 26 to 65

- Alignment No. 9110
- gi No. 1173219
- % Identity 72.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1105: from 26 to 65

- Alignment No. 9111
- gi No. 1173220
- % Identity 77.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1105: from 26 to 65

- Alignment No. 9112
- gi No. 133793
- % Identity 92.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1105: from 26 to 65

- Alignment No. 9113
- gi No. 133884
- % Identity 75
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1105: from 26 to 65

- Alignment No. 9114
- gi No. 1350954
- % Identity 77.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1105: from 26 to 65

- Alignment No. 9115
- gi No. 2130985
- % Identity 90
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1105: from 26 to 65

- Alignment No. 9116
- gi No. 2281972
- % Identity 72.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1105: from 26 to 65

- Alignment No. 9117
- gi No. 2429452
- % Identity 72.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1105: from 26 to 65

- Alignment No. 9118
- gi No. 3355488
- % Identity 88.6
- Alignment Length 44
- Location of Alignment in SEQ ID NO 1105: from 22 to 65

- Alignment No. 9119
- gi No. 3758866
- % Identity 76.3
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1105: from 26 to 63

- Alignment No. 9120

- gi No. 417715
- % Identity 70
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1105: from 26 to 65

- Alignment No. 9121
- gi No. 4506689
- % Identity 75
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1105: from 26 to 65

- Alignment No. 9122
- gi No. 464711
- % Identity 75
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1105: from 26 to 65

- Alignment No. 9123
- gi No. 5679124
- % Identity 77.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1105: from 26 to 65

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1106
- Ceres seq_id 1499657
- Location of start within SEQ ID NO 1104: at 78 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9124
- gi No. 1071974
- % Identity 72.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1106: from 1 to 40

- Alignment No. 9125
- gi No. 1173217
- % Identity 72.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1106: from 1 to 40

- Alignment No. 9126
- gi No. 1173218
- % Identity 95
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1106: from 1 to 40

- Alignment No. 9127
- gi No. 1173219
- % Identity 72.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1106: from 1 to 40

- Alignment No. 9128
- gi No. 1173220
- % Identity 77.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1106: from 1 to 40

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- Alignment No. 9129
- gi No. 133793
- % Identity 92.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1106: from 1 to 40

- Alignment No. 9130
- gi No. 133884
- % Identity 75
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1106: from 1 to 40

- Alignment No. 9131
- gi No. 1350954
- % Identity 77.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1106: from 1 to 40

- Alignment No. 9132
- gi No. 2130985
- % Identity 90
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1106: from 1 to 40

- Alignment No. 9133
- gi No. 2281972
- % Identity 72.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1106: from 1 to 40

- Alignment No. 9134
- gi No. 2429452
- % Identity 72.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1106: from 1 to 40

- Alignment No. 9135
- gi No. 3355488
- % Identity 88.6
- Alignment Length 44
- Location of Alignment in SEQ ID NO 1106: from 1 to 40

- Alignment No. 9136
- gi No. 3758866
- % Identity 76.3
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1106: from 1 to 38

- Alignment No. 9137
- gi No. 417715
- % Identity 70
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1106: from 1 to 40

- Alignment No. 9138
- gi No. 4506689
- % Identity 75
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1106: from 1 to 40

- Alignment No. 9139

- ```
- gi No. 464711
- % Identity 75
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1106: from 1 to 40

- Alignment No. 9140
- gi No. 5679124
- % Identity 77.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1106: from 1 to 40
```

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1107
- Ceres seq\_id 1499658
- Location of start within SEQ ID NO 1104: at 117 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

#### (D) Related Amino Acid Sequences

- ```
- Alignment No. 9141
- gi No. 1071974
- % Identity 72.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1107: from 1 to 27

- Alignment No. 9142
- gi No. 1173217
- % Identity 72.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1107: from 1 to 27

- Alignment No. 9143
- gi No. 1173218
- % Identity 95
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1107: from 1 to 27

- Alignment No. 9144
- gi No. 1173219
- % Identity 72.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1107: from 1 to 27

- Alignment No. 9145
- gi No. 1173220
- % Identity 77.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1107: from 1 to 27

- Alignment No. 9146
- gi No. 133793
- % Identity 92.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1107: from 1 to 27

- Alignment No. 9147
- gi No. 133884
- % Identity 75
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1107: from 1 to 27
```

- Alignment No. 9148
- gi No. 1350954
- % Identity 77.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1107: from 1 to 27

- Alignment No. 9149
- gi No. 2130985
- % Identity 90
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1107: from 1 to 27

- Alignment No. 9150
- gi No. 2281972
- % Identity 72.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1107: from 1 to 27

- Alignment No. 9151
- gi No. 2429452
- % Identity 72.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1107: from 1 to 27

- Alignment No. 9152
- gi No. 3355488
- % Identity 88.6
- Alignment Length 44
- Location of Alignment in SEQ ID NO 1107: from 1 to 27

- Alignment No. 9153
- gi No. 3758866
- % Identity 76.3
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1107: from 1 to 25

- Alignment No. 9154
- gi No. 417715
- % Identity 70
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1107: from 1 to 27

- Alignment No. 9155
- gi No. 4506689
- % Identity 75
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1107: from 1 to 27

- Alignment No. 9156
- gi No. 464711
- % Identity 75
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1107: from 1 to 27

- Alignment No. 9157
- gi No. 5679124
- % Identity 77.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1107: from 1 to 27

Maximum Length Sequence corresponding to clone ID 247264

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1108
- Ceres seq_id 1499667

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1109
- Ceres seq_id 1499668
- Location of start within SEQ ID NO 1108: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1110
- Ceres seq_id 1499669
- Location of start within SEQ ID NO 1108: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9158
- Uncharacterized protein family
- Location within SEQ ID NO 1110: from 81 to 166 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9159
- gi No. 4886288
- % Identity 86.1
- Alignment Length 79
- Location of Alignment in SEQ ID NO 1110: from 82 to 160

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1111
- Ceres seq_id 1499670
- Location of start within SEQ ID NO 1108: at 21 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9160
- Uncharacterized protein family
- Location within SEQ ID NO 1111: from 75 to 160 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9161
- gi No. 4886288
- % Identity 86.1
- Alignment Length 79
- Location of Alignment in SEQ ID NO 1111: from 76 to 154

Maximum Length Sequence corresponding to clone ID 247265

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1112
- Ceres seq_id 1499671

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1113
- Ceres seq_id 1499672
- Location of start within SEQ ID NO 1112: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1114
- Ceres seq_id 1499673
- Location of start within SEQ ID NO 1112: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9162
- gi No. 1523800
- % Identity 71.4
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1114: from 16 to 29
- Alignment No. 9163
- gi No. 3219273
- % Identity 71.4
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1114: from 16 to 29

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1115
- Ceres seq_id 1499674
- Location of start within SEQ ID NO 1112: at 193 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9164
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1115: from 21 to 115 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 247273

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1116
- Ceres seq_id 1499675

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1117
- Ceres seq_id 1499676
- Location of start within SEQ ID NO 1116: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9165
- gi No. 123704
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1117: from 52 to 70

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1118
- Ceres seq_id 1499677
- Location of start within SEQ ID NO 1116: at 92 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1119
- Ceres seq_id 1499678
- Location of start within SEQ ID NO 1116: at 115 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 247522

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1120
- Ceres seq_id 1499686

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1121
- Ceres seq_id 1499687
- Location of start within SEQ ID NO 1120: at 61 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9166
- Sugar (and other) transporter
- Location within SEQ ID NO 1121: from 24 to 142 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1122
- Ceres seq_id 1499688
- Location of start within SEQ ID NO 1120: at 148 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9167
- Sugar (and other) transporter
- Location within SEQ ID NO 1122: from 1 to 113 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1123
- Ceres seq_id 1499689
- Location of start within SEQ ID NO 1120: at 184 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9168
- Sugar (and other) transporter
- Location within SEQ ID NO 1123: from 1 to 101 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 247534

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1124
- Ceres seq_id 1499690

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1125
- Ceres seq_id 1499691
- Location of start within SEQ ID NO 1124: at 75 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9169
- 4 transmembrane segments integral membrane proteins
- Location within SEQ ID NO 1125: from 78 to 131 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1126
- Ceres seq_id 1499692
- Location of start within SEQ ID NO 1124: at 150 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9170
- 4 transmembrane segments integral membrane proteins
- Location within SEQ ID NO 1126: from 53 to 106 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1127
- Ceres seq_id 1499693
- Location of start within SEQ ID NO 1124: at 186 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9171
- 4 transmembrane segments integral membrane proteins
- Location within SEQ ID NO 1127: from 41 to 94 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 247548

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1128
- Ceres seq_id 1499694

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1129
- Ceres seq_id 1499695
- Location of start within SEQ ID NO 1128: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9172
- gi No. 1418990
- % Identity 70.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1129: from 70 to 93
- Alignment No. 9173
- gi No. 2443890
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1129: from 71 to 92
- Alignment No. 9174
- gi No. 2459430
- % Identity 73.1

- Alignment Length 26
- Location of Alignment in SEQ ID NO 1129: from 70 to 95

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1130
- Ceres seq_id 1499696
- Location of start within SEQ ID NO 1128: at 183 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9175
- gi No. 1418990
- % Identity 70.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1130: from 10 to 33
- Alignment No. 9176
- gi No. 2443890
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1130: from 11 to 32
- Alignment No. 9177
- gi No. 2459430
- % Identity 73.1
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1130: from 10 to 35

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1131
- Ceres seq_id 1499697
- Location of start within SEQ ID NO 1128: at 198 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9178
- gi No. 1418990
- % Identity 70.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1131: from 5 to 28
- Alignment No. 9179
- gi No. 2443890
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1131: from 6 to 27
- Alignment No. 9180
- gi No. 2459430
- % Identity 73.1
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1131: from 5 to 30

Maximum Length Sequence corresponding to clone ID 247645

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1132
- Ceres seq_id 1499720

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1133

- Ceres seq_id 1499721
- Location of start within SEQ ID NO 1132: at 118 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 9181
 - gi No. 4883616
 - % Identity 73.3
 - Alignment Length 60
 - Location of Alignment in SEQ ID NO 1133: from 57 to 116

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1134
- Ceres seq_id 1499722
- Location of start within SEQ ID NO 1132: at 172 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 9182
 - gi No. 4883616
 - % Identity 73.3
 - Alignment Length 60
 - Location of Alignment in SEQ ID NO 1134: from 39 to 98

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1135
- Ceres seq_id 1499723
- Location of start within SEQ ID NO 1132: at 214 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 9183
 - gi No. 4883616
 - % Identity 73.3
 - Alignment Length 60
 - Location of Alignment in SEQ ID NO 1135: from 25 to 84

Maximum Length Sequence corresponding to clone ID 247783

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1136
- Ceres seq_id 1499728

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1137
- Ceres seq_id 1499729
- Location of start within SEQ ID NO 1136: at 146 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9184
- tRNA pseudouridine synthase
- Location within SEQ ID NO 1137: from 46 to 146 aa.

- Alignment No. 9185
- tRNA pseudouridine synthase
- Location within SEQ ID NO 1137: from 256 to 355 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1138
- Ceres seq_id 1499730
- Location of start within SEQ ID NO 1136: at 257 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9186
- tRNA pseudouridine synthase
- Location within SEQ ID NO 1138: from 9 to 109 aa.
- Alignment No. 9187
- tRNA pseudouridine synthase
- Location within SEQ ID NO 1138: from 219 to 318 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1139
- Ceres seq_id 1499731
- Location of start within SEQ ID NO 1136: at 617 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9188
- tRNA pseudouridine synthase
- Location within SEQ ID NO 1139: from 99 to 198 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 247881

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1140
- Ceres seq_id 1499732

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1141
- Ceres seq_id 1499733
- Location of start within SEQ ID NO 1140: at 80 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9189
- Helix-loop-helix DNA-binding domain
- Location within SEQ ID NO 1141: from 134 to 181 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1142
- Ceres seq_id 1499734
- Location of start within SEQ ID NO 1140: at 89 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9190
- Helix-loop-helix DNA-binding domain
- Location within SEQ ID NO 1142: from 131 to 178 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1143
- Ceres seq_id 1499735
- Location of start within SEQ ID NO 1140: at 332 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9191
- Helix-loop-helix DNA-binding domain
- Location within SEQ ID NO 1143: from 50 to 97 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 248288

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1144
- Ceres seq_id 1499740

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1145
- Ceres seq_id 1499741
- Location of start within SEQ ID NO 1144: at 116 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1146
- Ceres seq_id 1499742
- Location of start within SEQ ID NO 1144: at 185 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1147
- Ceres seq_id 1499743
- Location of start within SEQ ID NO 1144: at 744 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9192
- Integral membrane protein
- Location within SEQ ID NO 1147: from 1 to 122 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 248560

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1148
- Ceres seq_id 1499748

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1149
- Ceres seq_id 1499749
- Location of start within SEQ ID NO 1148: at 89 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9193
- gi No. 3004561

- % Identity 100
- Alignment Length 125
- Location of Alignment in SEQ ID NO 1149: from 1 to 125

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1150
- Ceres seq_id 1499750
- Location of start within SEQ ID NO 1148: at 188 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9194
- gi No. 3004561
- % Identity 100
- Alignment Length 125
- Location of Alignment in SEQ ID NO 1150: from 1 to 92

Maximum Length Sequence corresponding to clone ID 248721

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1151
- Ceres seq_id 1499751

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1152
- Ceres seq_id 1499752
- Location of start within SEQ ID NO 1151: at 31 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9195
- gi No. 5262162
- % Identity 97.5
- Alignment Length 197
- Location of Alignment in SEQ ID NO 1152: from 1 to 197

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1153
- Ceres seq_id 1499753
- Location of start within SEQ ID NO 1151: at 112 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9196
- gi No. 5262162
- % Identity 97.5
- Alignment Length 197
- Location of Alignment in SEQ ID NO 1153: from 1 to 170

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1154
- Ceres seq_id 1499754
- Location of start within SEQ ID NO 1151: at 139 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9197
- gi No. 5262162
- % Identity 97.5

- Alignment Length 197
- Location of Alignment in SEQ ID NO 1154: from 1 to 161

Maximum Length Sequence corresponding to clone ID 248969

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1155
- Ceres seq_id 1499755

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1156
- Ceres seq_id 1499756
- Location of start within SEQ ID NO 1155: at 184 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1157
- Ceres seq_id 1499757
- Location of start within SEQ ID NO 1155: at 320 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9198
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1157: from 63 to 115 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 248974

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1158
- Ceres seq_id 1499758

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1159
- Ceres seq_id 1499759
- Location of start within SEQ ID NO 1158: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9199
- Ribosomal L10
- Location within SEQ ID NO 1159: from 19 to 70 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9200
- gi No. 1172806
- % Identity 92.3
- Alignment Length 52
- Location of Alignment in SEQ ID NO 1159: from 19 to 70

- Alignment No. 9201
- gi No. 1172807
- % Identity 78.7
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1159: from 19 to 65

- Alignment No. 9202
- gi No. 1172808
- % Identity 75.6
- Alignment Length 41

- ```

- Location of Alignment in SEQ ID NO 1159: from 25 to 65
- Alignment No. 9203
- gi No. 1172809
- % Identity 88.5
- Alignment Length 52
- Location of Alignment in SEQ ID NO 1159: from 19 to 70
- Alignment No. 9204
- gi No. 1172810
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1159: from 19 to 65
- Alignment No. 9205
- gi No. 1172811
- % Identity 88.5
- Alignment Length 52
- Location of Alignment in SEQ ID NO 1159: from 19 to 70
- Alignment No. 9206
- gi No. 1172812
- % Identity 74.5
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1159: from 19 to 65
- Alignment No. 9207
- gi No. 1172813
- % Identity 93.5
- Alignment Length 46
- Location of Alignment in SEQ ID NO 1159: from 19 to 64
- Alignment No. 9208
- gi No. 2317762
- % Identity 80.8
- Alignment Length 52
- Location of Alignment in SEQ ID NO 1159: from 19 to 70
- Alignment No. 9209
- gi No. 2500351
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1159: from 19 to 65
- Alignment No. 9210
- gi No. 2500352
- % Identity 70.2
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1159: from 19 to 65
- Alignment No. 9211
- gi No. 2500353
- % Identity 95.7
- Alignment Length 46
- Location of Alignment in SEQ ID NO 1159: from 19 to 64
- Alignment No. 9212
- gi No. 2500354
- % Identity 88.5
- Alignment Length 52
- Location of Alignment in SEQ ID NO 1159: from 19 to 70

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- Alignment No. 9213
- gi No. 2500356
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1159: from 19 to 65
  
- Alignment No. 9214
- gi No. 3123840
- % Identity 74.5
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1159: from 19 to 65
  
- Alignment No. 9215
- gi No. 4063389
- % Identity 78.7
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1159: from 19 to 65
  
- Alignment No. 9216
- gi No. 4107323
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1159: from 19 to 65
  
- Alignment No. 9217
- gi No. 4262180
- % Identity 92.3
- Alignment Length 52
- Location of Alignment in SEQ ID NO 1159: from 19 to 70
  
- Alignment No. 9218
- gi No. 4493745
- % Identity 72.3
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1159: from 19 to 65
  
- Alignment No. 9219
- gi No. 4929242
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1159: from 19 to 65
  
- Alignment No. 9220
- gi No. 5174431
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1159: from 19 to 65
  
- Alignment No. 9221
- gi No. 88079
- % Identity 77.1
- Alignment Length 48
- Location of Alignment in SEQ ID NO 1159: from 18 to 65

(B) Polypeptide Sequence

- ```
- Pat. Appln. SEQ ID NO 1160
- Ceres seq_id 1499760
- Location of start within SEQ ID NO 1158: at 56 nt.
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(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

- Alignment No. 9222
- Ribosomal L10
- Location within SEQ ID NO 1160: from 1 to 52 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9223
- gi No. 1172806
- % Identity 92.3
- Alignment Length 52
- Location of Alignment in SEQ ID NO 1160: from 1 to 52
- Alignment No. 9224
- gi No. 1172807
- % Identity 78.7
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1160: from 1 to 47
- Alignment No. 9225
- gi No. 1172808
- % Identity 75.6
- Alignment Length 41
- Location of Alignment in SEQ ID NO 1160: from 7 to 47
- Alignment No. 9226
- gi No. 1172809
- % Identity 88.5
- Alignment Length 52
- Location of Alignment in SEQ ID NO 1160: from 1 to 52
- Alignment No. 9227
- gi No. 1172810
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1160: from 1 to 47
- Alignment No. 9228
- gi No. 1172811
- % Identity 88.5
- Alignment Length 52
- Location of Alignment in SEQ ID NO 1160: from 1 to 52
- Alignment No. 9229
- gi No. 1172812
- % Identity 74.5
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1160: from 1 to 47
- Alignment No. 9230
- gi No. 1172813
- % Identity 93.5
- Alignment Length 46
- Location of Alignment in SEQ ID NO 1160: from 1 to 46
- Alignment No. 9231
- gi No. 2317762
- % Identity 80.8
- Alignment Length 52
- Location of Alignment in SEQ ID NO 1160: from 1 to 52

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- Alignment No. 9232
- gi No. 2500351
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1160: from 1 to 47

- Alignment No. 9233
- gi No. 2500352
- % Identity 70.2
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1160: from 1 to 47

- Alignment No. 9234
- gi No. 2500353
- % Identity 95.7
- Alignment Length 46
- Location of Alignment in SEQ ID NO 1160: from 1 to 46

- Alignment No. 9235
- gi No. 2500354
- % Identity 88.5
- Alignment Length 52
- Location of Alignment in SEQ ID NO 1160: from 1 to 52

- Alignment No. 9236
- gi No. 2500356
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1160: from 1 to 47

- Alignment No. 9237
- gi No. 3123840
- % Identity 74.5
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1160: from 1 to 47

- Alignment No. 9238
- gi No. 4063389
- % Identity 78.7
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1160: from 1 to 47

- Alignment No. 9239
- gi No. 4107323
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1160: from 1 to 47

- Alignment No. 9240
- gi No. 4262180
- % Identity 92.3
- Alignment Length 52
- Location of Alignment in SEQ ID NO 1160: from 1 to 52

- Alignment No. 9241
- gi No. 4493745
- % Identity 72.3
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1160: from 1 to 47

- Alignment No. 9242

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- gi No. 4929242
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1160: from 1 to 47

- Alignment No. 9243
- gi No. 5174431
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1160: from 1 to 47

- Alignment No. 9244
- gi No. 88079
- % Identity 77.1
- Alignment Length 48
- Location of Alignment in SEQ ID NO 1160: from 1 to 47

Maximum Length Sequence corresponding to clone ID 249321

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1161
- Ceres seq_id 1499765

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1162
- Ceres seq_id 1499766
- Location of start within SEQ ID NO 1161: at 608 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9245
- gi No. 123530
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1162: from 29 to 39

- Alignment No. 9246
- gi No. 3875708
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1162: from 4 to 14

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1163
- Ceres seq_id 1499767
- Location of start within SEQ ID NO 1161: at 773 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1164
- Ceres seq_id 1499768
- Location of start within SEQ ID NO 1161: at 777 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 249331

(A) Polynucleotide Sequence

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- Pat. Appln. SEQ ID NO 1165
- Ceres seq_id 1499769

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1166
- Ceres seq_id 1499770
- Location of start within SEQ ID NO 1165: at 68 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9247
- gi No. 4972053
- % Identity 90.4
- Alignment Length 115
- Location of Alignment in SEQ ID NO 1166: from 1 to 102

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1167
- Ceres seq_id 1499771
- Location of start within SEQ ID NO 1165: at 131 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9248
- gi No. 4972053
- % Identity 90.4
- Alignment Length 115
- Location of Alignment in SEQ ID NO 1167: from 1 to 81

Maximum Length Sequence corresponding to clone ID 249334

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1168
- Ceres seq_id 1499772

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1169
- Ceres seq_id 1499773
- Location of start within SEQ ID NO 1168: at 159 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9249
- alpha/beta hydrolase fold
- Location within SEQ ID NO 1169: from 180 to 249 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 249340

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1170
- Ceres seq_id 1499777

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1171
- Ceres seq_id 1499778
- Location of start within SEQ ID NO 1170: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9250
- gi No. 1531760

- % Identity 99.3
- Alignment Length 273
- Location of Alignment in SEQ ID NO 1171: from 40 to 312
- Alignment No. 9251
- gi No. 1778015
- % Identity 98.5
- Alignment Length 273
- Location of Alignment in SEQ ID NO 1171: from 40 to 312
- Alignment No. 9252
- gi No. 1817544
- % Identity 99.6
- Alignment Length 273
- Location of Alignment in SEQ ID NO 1171: from 40 to 312
- Alignment No. 9253
- gi No. 4164139
- % Identity 100
- Alignment Length 19
- Location of Alignment in SEQ ID NO 1171: from 40 to 58

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1172
- Ceres seq_id 1499779
- Location of start within SEQ ID NO 1170: at 120 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9254
- gi No. 1531760
- % Identity 99.3
- Alignment Length 273
- Location of Alignment in SEQ ID NO 1172: from 1 to 273
- Alignment No. 9255
- gi No. 1778015
- % Identity 98.5
- Alignment Length 273
- Location of Alignment in SEQ ID NO 1172: from 1 to 273
- Alignment No. 9256
- gi No. 1817544
- % Identity 99.6
- Alignment Length 273
- Location of Alignment in SEQ ID NO 1172: from 1 to 273
- Alignment No. 9257
- gi No. 4164139
- % Identity 100
- Alignment Length 19
- Location of Alignment in SEQ ID NO 1172: from 1 to 19

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1173
- Ceres seq_id 1499780
- Location of start within SEQ ID NO 1170: at 402 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9258
- gi No. 1531760
- % Identity 99.3
- Alignment Length 273
- Location of Alignment in SEQ ID NO 1173: from 1 to 179

- Alignment No. 9259
- gi No. 1778015
- % Identity 98.5
- Alignment Length 273
- Location of Alignment in SEQ ID NO 1173: from 1 to 179

- Alignment No. 9260
- gi No. 1817544
- % Identity 99.6
- Alignment Length 273
- Location of Alignment in SEQ ID NO 1173: from 1 to 179

Maximum Length Sequence corresponding to clone ID 249370

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1174
- Ceres seq_id 1499785

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1175
- Ceres seq_id 1499786
- Location of start within SEQ ID NO 1174: at 50 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9261
- Zinc-binding dehydrogenases
- Location within SEQ ID NO 1175: from 73 to 167 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1176
- Ceres seq_id 1499787
- Location of start within SEQ ID NO 1174: at 62 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9262
- Zinc-binding dehydrogenases
- Location within SEQ ID NO 1176: from 69 to 163 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1177
- Ceres seq_id 1499788
- Location of start within SEQ ID NO 1174: at 170 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9263
- Zinc-binding dehydrogenases
- Location within SEQ ID NO 1177: from 33 to 127 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 249388

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1178
- Ceres seq_id 1499789

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1179
- Ceres seq_id 1499790
- Location of start within SEQ ID NO 1178: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9264
- Merozoite Surface Antigen 2 (MSA-2) family
- Location within SEQ ID NO 1179: from 110 to 240 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1180
- Ceres seq_id 1499791
- Location of start within SEQ ID NO 1178: at 120 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9265
- Merozoite Surface Antigen 2 (MSA-2) family
- Location within SEQ ID NO 1180: from 71 to 201 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 249485

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1181
- Ceres seq_id 1499792

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1182
- Ceres seq_id 1499793
- Location of start within SEQ ID NO 1181: at 154 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9266
- Dehydrogenase E1 component
- Location within SEQ ID NO 1182: from 73 to 377 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9267
- gi No. 2454182
- % Identity 98.9
- Alignment Length 366
- Location of Alignment in SEQ ID NO 1182: from 47 to 412

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1183
- Ceres seq_id 1499794
- Location of start within SEQ ID NO 1181: at 163 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9268

- Dehydrogenase E1 component
- Location within SEQ ID NO 1183: from 70 to 374 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9269
- gi No. 2454182
- % Identity 98.9
- Alignment Length 366
- Location of Alignment in SEQ ID NO 1183: from 44 to 409

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1184
- Ceres seq_id 1499795
- Location of start within SEQ ID NO 1181: at 376 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9270
- Dehydrogenase E1 component
- Location within SEQ ID NO 1184: from 1 to 303 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9271
- gi No. 2454182
- % Identity 98.9
- Alignment Length 366
- Location of Alignment in SEQ ID NO 1184: from 1 to 338

Maximum Length Sequence corresponding to clone ID 249591

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1185
- Ceres seq_id 1499800

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1186
- Ceres seq_id 1499801
- Location of start within SEQ ID NO 1185: at 335 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9272
- gi No. 2708751
- % Identity 83.1
- Alignment Length 267
- Location of Alignment in SEQ ID NO 1186: from 32 to 292

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1187
- Ceres seq_id 1499802
- Location of start within SEQ ID NO 1185: at 338 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9273
- gi No. 2708751
- % Identity 83.1
- Alignment Length 267
- Location of Alignment in SEQ ID NO 1187: from 31 to 291

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1188
- Ceres seq_id 1499803
- Location of start within SEQ ID NO 1185: at 362 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 9274
 - gi No. 2708751
 - % Identity 83.1
 - Alignment Length 267
 - Location of Alignment in SEQ ID NO 1188: from 23 to 283

Maximum Length Sequence corresponding to clone ID 249631

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1189
- Ceres seq_id 1499811

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1190
- Ceres seq_id 1499812
- Location of start within SEQ ID NO 1189: at 381 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9275
- Phosphoglycerate mutase family
- Location within SEQ ID NO 1190: from 1 to 78 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9276
- gi No. 4539345
- % Identity 99.2
- Alignment Length 124
- Location of Alignment in SEQ ID NO 1190: from 1 to 123

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1191
- Ceres seq_id 1499813
- Location of start within SEQ ID NO 1189: at 384 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9277
- Phosphoglycerate mutase family
- Location within SEQ ID NO 1191: from 1 to 77 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9278
- gi No. 4539345
- % Identity 99.2
- Alignment Length 124
- Location of Alignment in SEQ ID NO 1191: from 1 to 122

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1192
- Ceres seq_id 1499814
- Location of start within SEQ ID NO 1189: at 483 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9279
- gi No. 4539345
- % Identity 99.2
- Alignment Length 124
- Location of Alignment in SEQ ID NO 1192: from 1 to 89

Maximum Length Sequence corresponding to clone ID 249747

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1193
- Ceres seq_id 1499823

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1194
- Ceres seq_id 1499824
- Location of start within SEQ ID NO 1193: at 131 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9280
- Tropomyosins
- Location within SEQ ID NO 1194: from 126 to 244 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9281
- gi No. 2832682
- % Identity 96.3
- Alignment Length 244
- Location of Alignment in SEQ ID NO 1194: from 1 to 244

Maximum Length Sequence corresponding to clone ID 249756

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1195
- Ceres seq_id 1499825

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1196
- Ceres seq_id 1499826
- Location of start within SEQ ID NO 1195: at 208 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9282
- Protein phosphatase 2C
- Location within SEQ ID NO 1196: from 243 to 317 aa.

- Alignment No. 9283
- Protein phosphatase 2C
- Location within SEQ ID NO 1196: from 309 to 452 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1197
- Ceres seq_id 1499827
- Location of start within SEQ ID NO 1195: at 535 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9284
- Protein phosphatase 2C
- Location within SEQ ID NO 1197: from 134 to 208 aa.

- Alignment No. 9285

- Protein phosphatase 2C
- Location within SEQ ID NO 1197: from 200 to 343 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1198
- Ceres seq_id 1499828
- Location of start within SEQ ID NO 1195: at 607 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9286
- Protein phosphatase 2C
- Location within SEQ ID NO 1198: from 110 to 184 aa.
- Alignment No. 9287
- Protein phosphatase 2C
- Location within SEQ ID NO 1198: from 176 to 319 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 249769

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1199
- Ceres seq_id 1499829

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1200
- Ceres seq_id 1499830
- Location of start within SEQ ID NO 1199: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9288
- gi No. 4914402
- % Identity 99.6
- Alignment Length 515
- Location of Alignment in SEQ ID NO 1200: from 17 to 531

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1201
- Ceres seq_id 1499831
- Location of start within SEQ ID NO 1199: at 50 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9289
- gi No. 4914402
- % Identity 99.6
- Alignment Length 515
- Location of Alignment in SEQ ID NO 1201: from 1 to 515

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1202
- Ceres seq_id 1499832
- Location of start within SEQ ID NO 1199: at 338 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 9290
 - gi No. 4914402
 - % Identity 99.6
 - Alignment Length 515
 - Location of Alignment in SEQ ID NO 1202: from 1 to 419

Maximum Length Sequence corresponding to clone ID 249772

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1203
 - Ceres seq_id 1499833
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1204
 - Ceres seq_id 1499834
 - Location of start within SEQ ID NO 1203: at 70 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9291
- Mitochondrial carrier proteins
- Location within SEQ ID NO 1204: from 121 to 388 aa.

- (D) Related Amino Acid Sequences
 - Alignment No. 9292
 - gi No. 3068714
 - % Identity 75.5
 - Alignment Length 343
 - Location of Alignment in SEQ ID NO 1204: from 64 to 405

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1205
 - Ceres seq_id 1499835
 - Location of start within SEQ ID NO 1203: at 496 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9293
- Mitochondrial carrier proteins
- Location within SEQ ID NO 1205: from 1 to 246 aa.

- (D) Related Amino Acid Sequences
 - Alignment No. 9294
 - gi No. 3068714
 - % Identity 75.5
 - Alignment Length 343
 - Location of Alignment in SEQ ID NO 1205: from 1 to 263

Maximum Length Sequence corresponding to clone ID 249844

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1206
 - Ceres seq_id 1499844
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1207
 - Ceres seq_id 1499845
 - Location of start within SEQ ID NO 1206: at 174 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9295
- Tropomyosins
- Location within SEQ ID NO 1207: from 122 to 242 aa.

- (D) Related Amino Acid Sequences
 - Alignment No. 9296
 - gi No. 2832682
 - % Identity 96.7
 - Alignment Length 242
 - Location of Alignment in SEQ ID NO 1207: from 1 to 242

Maximum Length Sequence corresponding to clone ID 250092

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1208
 - Ceres seq_id 1499850
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1209
 - Ceres seq_id 1499851
 - Location of start within SEQ ID NO 1208: at 78 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1210
 - Ceres seq_id 1499852
 - Location of start within SEQ ID NO 1208: at 190 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 9297
 - gi No. 4097571
 - % Identity 76.9
 - Alignment Length 13
 - Location of Alignment in SEQ ID NO 1210: from 91 to 103

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1211
 - Ceres seq_id 1499853
 - Location of start within SEQ ID NO 1208: at 362 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 250127

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1212
 - Ceres seq_id 1499854
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1213
 - Ceres seq_id 1499855
 - Location of start within SEQ ID NO 1212: at 135 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9298
- Zinc finger, C3HC4 type (RING finger)
- Location within SEQ ID NO 1213: from 113 to 153 aa.

- (D) Related Amino Acid Sequences

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(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1214
- Ceres seq_id 1499856
- Location of start within SEQ ID NO 1212: at 330 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9299
- Zinc finger, C3HC4 type (RING finger)
- Location within SEQ ID NO 1214: from 48 to 88 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1215
- Ceres seq_id 1499857
- Location of start within SEQ ID NO 1212: at 357 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9300
- Zinc finger, C3HC4 type (RING finger)
- Location within SEQ ID NO 1215: from 39 to 79 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 250751

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1216
- Ceres seq_id 1499875

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1217
- Ceres seq_id 1499876
- Location of start within SEQ ID NO 1216: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9301
- gi No. 1698582
- % Identity 74.2
- Alignment Length 376
- Location of Alignment in SEQ ID NO 1217: from 62 to 435

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1218
- Ceres seq_id 1499877
- Location of start within SEQ ID NO 1216: at 35 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9302
- gi No. 1698582
- % Identity 74.2
- Alignment Length 376
- Location of Alignment in SEQ ID NO 1218: from 51 to 424

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1219
- Ceres seq_id 1499878

- Location of start within SEQ ID NO 1216: at 404 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9303
- gi No. 1698582
- % Identity 74.2
- Alignment Length 376
- Location of Alignment in SEQ ID NO 1219: from 1 to 301

Maximum Length Sequence corresponding to clone ID 251247

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1220
- Ceres seq_id 1499899

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1221
- Ceres seq_id 1499900
- Location of start within SEQ ID NO 1220: at 96 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9304
- Response regulator receiver domain
- Location within SEQ ID NO 1221: from 22 to 136 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9305
- gi No. 3687688
- % Identity 78.9
- Alignment Length 142
- Location of Alignment in SEQ ID NO 1221: from 1 to 142

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1222
- Ceres seq_id 1499901
- Location of start within SEQ ID NO 1220: at 210 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9306
- Response regulator receiver domain
- Location within SEQ ID NO 1222: from 1 to 98 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9307
- gi No. 3687688
- % Identity 78.9
- Alignment Length 142
- Location of Alignment in SEQ ID NO 1222: from 1 to 104

Maximum Length Sequence corresponding to clone ID 251438

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1223
- Ceres seq_id 1499902

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1224
- Ceres seq_id 1499903
- Location of start within SEQ ID NO 1223: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9308
- alpha/beta hydrolase fold
- Location within SEQ ID NO 1224: from 73 to 136 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1225
- Ceres seq_id 1499904
- Location of start within SEQ ID NO 1223: at 70 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9309
- alpha/beta hydrolase fold
- Location within SEQ ID NO 1225: from 50 to 113 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1226
- Ceres seq_id 1499905
- Location of start within SEQ ID NO 1223: at 163 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9310
- alpha/beta hydrolase fold
- Location within SEQ ID NO 1226: from 19 to 82 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 251466

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1227
- Ceres seq_id 1499906

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1228
- Ceres seq_id 1499907
- Location of start within SEQ ID NO 1227: at 53 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9311
- AP2 domain
- Location within SEQ ID NO 1228: from 62 to 112 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9312
- gi No. 1246403
- % Identity 74.5
- Alignment Length 55
- Location of Alignment in SEQ ID NO 1228: from 59 to 112
- Alignment No. 9313
- gi No. 3643601
- % Identity 70
- Alignment Length 50
- Location of Alignment in SEQ ID NO 1228: from 64 to 112

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1229
 - Ceres seq_id 1499908
 - Location of start within SEQ ID NO 1227: at 490 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 251549

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1230
 - Ceres seq_id 1499909
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1231
 - Ceres seq_id 1499910
 - Location of start within SEQ ID NO 1230: at 430 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 9314
 - gi No. 4982498
 - % Identity 100
 - Alignment Length 154
 - Location of Alignment in SEQ ID NO 1231: from 6 to 159

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1232
 - Ceres seq_id 1499911
 - Location of start within SEQ ID NO 1230: at 439 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 9315
 - gi No. 4982498
 - % Identity 100
 - Alignment Length 154
 - Location of Alignment in SEQ ID NO 1232: from 3 to 156

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1233
 - Ceres seq_id 1499912
 - Location of start within SEQ ID NO 1230: at 466 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 9316
 - gi No. 4982498
 - % Identity 100
 - Alignment Length 154
 - Location of Alignment in SEQ ID NO 1233: from 1 to 147

Maximum Length Sequence corresponding to clone ID 251841

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1234
 - Ceres seq_id 1499924
- (B) Polypeptide Sequence

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- Pat. Appln. SEQ ID NO 1235
- Ceres seq_id 1499925
- Location of start within SEQ ID NO 1234: at 21 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9317
- RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- Location within SEQ ID NO 1235: from 46 to 113 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9318
- gi No. 2827657
- % Identity 96.3
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1235: from 46 to 152

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1236
- Ceres seq_id 1499926
- Location of start within SEQ ID NO 1234: at 147 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9319
- RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- Location within SEQ ID NO 1236: from 4 to 71 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9320
- gi No. 2827657
- % Identity 96.3
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1236: from 4 to 110

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1237
- Ceres seq_id 1499927
- Location of start within SEQ ID NO 1234: at 249 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9321
- gi No. 2827657
- % Identity 96.3
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1237: from 1 to 76

Maximum Length Sequence corresponding to clone ID 251906

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1238
- Ceres seq_id 1499928

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1239
- Ceres seq_id 1499929
- Location of start within SEQ ID NO 1238: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9322

- Pollen proteins Ole e I family
- Location within SEQ ID NO 1239: from 48 to 108 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1240
- Ceres seq_id 1499930
- Location of start within SEQ ID NO 1238: at 51 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9323
- Pollen proteins Ole e I family
- Location within SEQ ID NO 1240: from 32 to 92 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1241
- Ceres seq_id 1499931
- Location of start within SEQ ID NO 1238: at 66 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9324
- Pollen proteins Ole e I family
- Location within SEQ ID NO 1241: from 27 to 87 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 252299

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1242
- Ceres seq_id 1499935

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1243
- Ceres seq_id 1499936
- Location of start within SEQ ID NO 1242: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9325
- Chlorophyll A-B binding proteins
- Location within SEQ ID NO 1243: from 62 to 114 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9326
- gi No. 100607
- % Identity 95
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1243: from 94 to 113
- Alignment No. 9327
- gi No. 1084336
- % Identity 87.5
- Alignment Length 96
- Location of Alignment in SEQ ID NO 1243: from 20 to 114
- Alignment No. 9328
- gi No. 115764

- % Identity 70.4
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1243: from 87 to 113

- Alignment No. 9329
- gi No. 115833
- % Identity 95
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1243: from 94 to 113

- Alignment No. 9330
- gi No. 115834
- % Identity 100
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1243: from 94 to 113

- Alignment No. 9331
- gi No. 2326947
- % Identity 74.2
- Alignment Length 31
- Location of Alignment in SEQ ID NO 1243: from 83 to 113

- Alignment No. 9332
- gi No. 2498362
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1243: from 98 to 112

- Alignment No. 9333
- gi No. 282865
- % Identity 74.1
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1243: from 87 to 113

- Alignment No. 9334
- gi No. 322377
- % Identity 94.1
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1243: from 96 to 112

- Alignment No. 9335
- gi No. 322380
- % Identity 74.1
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1243: from 84 to 110

- Alignment No. 9336
- gi No. 322392
- % Identity 73.1
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1243: from 87 to 112

- Alignment No. 9337
- gi No. 322393
- % Identity 73.1
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1243: from 87 to 112

- Alignment No. 9338
- gi No. 543939
- % Identity 100

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- Alignment No. 9345
- gi No. 100607
- % Identity 95
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1244: from 91 to 110

- Alignment No. 9346
- gi No. 1084336
- % Identity 87.5
- Alignment Length 96
- Location of Alignment in SEQ ID NO 1244: from 17 to 111

- Alignment No. 9347
- gi No. 115764
- % Identity 70.4
- Alignment Length 27

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- Location of Alignment in SEQ ID NO 1244: from 84 to 110
- Alignment No. 9348
 - gi No. 115833
 - % Identity 95
 - Alignment Length 20
 - Location of Alignment in SEQ ID NO 1244: from 91 to 110
- Alignment No. 9349
 - gi No. 115834
 - % Identity 100
 - Alignment Length 20
 - Location of Alignment in SEQ ID NO 1244: from 91 to 110
- Alignment No. 9350
 - gi No. 2326947
 - % Identity 74.2
 - Alignment Length 31
 - Location of Alignment in SEQ ID NO 1244: from 80 to 110
- Alignment No. 9351
 - gi No. 2498362
 - % Identity 73.3
 - Alignment Length 15
 - Location of Alignment in SEQ ID NO 1244: from 95 to 109
- Alignment No. 9352
 - gi No. 282865
 - % Identity 74.1
 - Alignment Length 27
 - Location of Alignment in SEQ ID NO 1244: from 84 to 110
- Alignment No. 9353
 - gi No. 322377
 - % Identity 94.1
 - Alignment Length 17
 - Location of Alignment in SEQ ID NO 1244: from 93 to 109
- Alignment No. 9354
 - gi No. 322380
 - % Identity 74.1
 - Alignment Length 27
 - Location of Alignment in SEQ ID NO 1244: from 81 to 107
- Alignment No. 9355
 - gi No. 322392
 - % Identity 73.1
 - Alignment Length 26
 - Location of Alignment in SEQ ID NO 1244: from 84 to 109
- Alignment No. 9356
 - gi No. 322393
 - % Identity 73.1
 - Alignment Length 26
 - Location of Alignment in SEQ ID NO 1244: from 84 to 109
- Alignment No. 9357
 - gi No. 543939
 - % Identity 100
 - Alignment Length 20
 - Location of Alignment in SEQ ID NO 1244: from 91 to 110

- ```
- Alignment No. 9358
- gi No. 625547
- % Identity 74.1
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1244: from 84 to 110

- Alignment No. 9359
- gi No. 82078
- % Identity 74.1
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1244: from 84 to 110

- Alignment No. 9360
- gi No. 82079
- % Identity 74.1
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1244: from 84 to 110

- Alignment No. 9361
- gi No. 99485
- % Identity 70.4
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1244: from 84 to 110

- Alignment No. 9362
- gi No. 99488
- % Identity 70.4
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1244: from 84 to 110
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(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1245
- Ceres seq\_id 1499938
- Location of start within SEQ ID NO 1242: at 532 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9363
- Chlorophyll A-B binding proteins
- Location within SEQ ID NO 1245: from 1 to 111 aa.

#### (D) Related Amino Acid Sequences

- ```
- Alignment No. 9364
- gi No. 1084336
- % Identity 97.2
- Alignment Length 143
- Location of Alignment in SEQ ID NO 1245: from 1 to 113
```

Maximum Length Sequence corresponding to clone ID 252372

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1246
- Ceres seq id 1499939

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1247
- Ceres seq_id 1499940
- Location of start within SEQ ID NO 1246: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9365
- gi No. 3169182
- % Identity 83.3
- Alignment Length 78
- Location of Alignment in SEQ ID NO 1247: from 46 to 122
- Alignment No. 9366
- gi No. 3860323
- % Identity 87.2
- Alignment Length 78
- Location of Alignment in SEQ ID NO 1247: from 46 to 122

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1248
- Ceres seq_id 1499941
- Location of start within SEQ ID NO 1246: at 138 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9367
- gi No. 3169182
- % Identity 83.3
- Alignment Length 78
- Location of Alignment in SEQ ID NO 1248: from 1 to 77
- Alignment No. 9368
- gi No. 3860323
- % Identity 87.2
- Alignment Length 78
- Location of Alignment in SEQ ID NO 1248: from 1 to 77

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1249
- Ceres seq_id 1499942
- Location of start within SEQ ID NO 1246: at 168 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9369
- gi No. 3169182
- % Identity 83.3
- Alignment Length 78
- Location of Alignment in SEQ ID NO 1249: from 1 to 67
- Alignment No. 9370
- gi No. 3860323
- % Identity 87.2
- Alignment Length 78
- Location of Alignment in SEQ ID NO 1249: from 1 to 67

Maximum Length Sequence corresponding to clone ID 252497

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1250
- Ceres seq_id 1499943

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1251
- Ceres seq_id 1499944
- Location of start within SEQ ID NO 1250: at 89 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

- Alignment No. 9371
- Core histone H2A/H2B/H3/H4
- Location within SEQ ID NO 1251: from 17 to 128 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9372
- gi No. 10253
- % Identity 88.3
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
- Alignment No. 9373
- gi No. 103198
- % Identity 90.6
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
- Alignment No. 9374
- gi No. 104698
- % Identity 88
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1251: from 2 to 26
- Alignment No. 9375
- gi No. 1053045
- % Identity 94.5
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1251: from 1 to 127
- Alignment No. 9376
- gi No. 1053047
- % Identity 94.5
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1251: from 1 to 127
- Alignment No. 9377
- gi No. 1053053
- % Identity 89.8
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1251: from 1 to 127
- Alignment No. 9378
- gi No. 1053055
- % Identity 82.8
- Alignment Length 29
- Location of Alignment in SEQ ID NO 1251: from 1 to 29
- Alignment No. 9379
- gi No. 1053057
- % Identity 94.5
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1251: from 1 to 127
- Alignment No. 9380
- gi No. 1053059
- % Identity 92.9
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1251: from 1 to 127

- Alignment No. 9381
- gi No. 1076583
- % Identity 95
- Alignment Length 60
- Location of Alignment in SEQ ID NO 1251: from 1 to 60

- Alignment No. 9382
- gi No. 1079199
- % Identity 90.6
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9383
- gi No. 1085857
- % Identity 91.6
- Alignment Length 83
- Location of Alignment in SEQ ID NO 1251: from 34 to 116

- Alignment No. 9384
- gi No. 1085858
- % Identity 92.8
- Alignment Length 83
- Location of Alignment in SEQ ID NO 1251: from 34 to 116

- Alignment No. 9385
- gi No. 108593
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1251: from 112 to 128

- Alignment No. 9386
- gi No. 109977
- % Identity 88.6
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1251: from 2 to 36

- Alignment No. 9387
- gi No. 1166436
- % Identity 81.4
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1251: from 36 to 94

- Alignment No. 9388
- gi No. 1197519
- % Identity 82.8
- Alignment Length 116
- Location of Alignment in SEQ ID NO 1251: from 13 to 128

- Alignment No. 9389
- gi No. 1208642
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1251: from 25 to 80

- Alignment No. 9390
- gi No. 1208644
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1251: from 25 to 80

- Alignment No. 9391

- gi No. 1208646
- % Identity 98.2
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1251: from 25 to 80

- Alignment No. 9392
- gi No. 1208656
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1251: from 25 to 80

- Alignment No. 9393
- gi No. 1208658
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1251: from 25 to 80

- Alignment No. 9394
- gi No. 1208664
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1251: from 25 to 80

- Alignment No. 9395
- gi No. 1208668
- % Identity 94.6
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1251: from 25 to 80

- Alignment No. 9396
- gi No. 1208699
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1251: from 25 to 80

- Alignment No. 9397
- gi No. 1208701
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1251: from 25 to 80

- Alignment No. 9398
- gi No. 1208707
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1251: from 25 to 80

- Alignment No. 9399
- gi No. 1208715
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1251: from 25 to 80

- Alignment No. 9400
- gi No. 1208725
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1251: from 25 to 80

- Alignment No. 9401
- gi No. 1208727

- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1251: from 25 to 80

- Alignment No. 9402
- gi No. 1213291
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1251: from 25 to 80

- Alignment No. 9403
- gi No. 1213307
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1251: from 25 to 80

- Alignment No. 9404
- gi No. 1213313
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1251: from 25 to 80

- Alignment No. 9405
- gi No. 1213315
- % Identity 89.3
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1251: from 25 to 80

- Alignment No. 9406
- gi No. 122065
- % Identity 87.5
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9407
- gi No. 122066
- % Identity 83.6
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9408
- gi No. 122068
- % Identity 91.4
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9409
- gi No. 122070
- % Identity 90.6
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9410
- gi No. 122071
- % Identity 82.9
- Alignment Length 41
- Location of Alignment in SEQ ID NO 1251: from 1 to 41

- Alignment No. 9411
- gi No. 122072
- % Identity 78

- Alignment Length 41
- Location of Alignment in SEQ ID NO 1251: from 1 to 41

- Alignment No. 9412
- gi No. 122074
- % Identity 87.5
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9413
- gi No. 122076
- % Identity 86.7
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9414
- gi No. 122077
- % Identity 84.3
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1251: from 1 to 127

- Alignment No. 9415
- gi No. 122078
- % Identity 77.3
- Alignment Length 132
- Location of Alignment in SEQ ID NO 1251: from 1 to 132

- Alignment No. 9416
- gi No. 122079
- % Identity 91.4
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9417
- gi No. 122080
- % Identity 85.2
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9418
- gi No. 122081
- % Identity 89.8
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9419
- gi No. 122082
- % Identity 89.8
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9420
- gi No. 122083
- % Identity 91.3
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1251: from 2 to 128

- Alignment No. 9421
- gi No. 122084
- % Identity 95.8
- Alignment Length 72

- Location of Alignment in SEQ ID NO 1251: from 57 to 128
- Alignment No. 9422
- gi No. 122085
- % Identity 92.2
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
- Alignment No. 9423
- gi No. 122086
- % Identity 84.4
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
- Alignment No. 9424
- gi No. 122087
- % Identity 92.2
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
- Alignment No. 9425
- gi No. 122088
- % Identity 90.6
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
- Alignment No. 9426
- gi No. 122089
- % Identity 89.8
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
- Alignment No. 9427
- gi No. 122090
- % Identity 92.2
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
- Alignment No. 9428
- gi No. 122091
- % Identity 84.4
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
- Alignment No. 9429
- gi No. 1360625
- % Identity 78.6
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1251: from 1 to 129
- Alignment No. 9430
- gi No. 1360627
- % Identity 76.5
- Alignment Length 98
- Location of Alignment in SEQ ID NO 1251: from 1 to 96
- Alignment No. 9431
- gi No. 1362108
- % Identity 92.1
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1251: from 1 to 127

- Alignment No. 9432
- gi No. 1362171
- % Identity 95.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1251: from 105 to 128
- Alignment No. 9433
- gi No. 159967
- % Identity 89.1
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
- Alignment No. 9434
- gi No. 161319
- % Identity 89.8
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
- Alignment No. 9435
- gi No. 166384
- % Identity 91.4
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
- Alignment No. 9436
- gi No. 1708108
- % Identity 92.2
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
- Alignment No. 9437
- gi No. 1708109
- % Identity 90.6
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
- Alignment No. 9438
- gi No. 171637
- % Identity 84.8
- Alignment Length 33
- Location of Alignment in SEQ ID NO 1251: from 3 to 35
- Alignment No. 9439
- gi No. 1723293
- % Identity 90.4
- Alignment Length 83
- Location of Alignment in SEQ ID NO 1251: from 46 to 128
- Alignment No. 9440
- gi No. 1731925
- % Identity 90.4
- Alignment Length 115
- Location of Alignment in SEQ ID NO 1251: from 3 to 117
- Alignment No. 9441
- gi No. 1762791
- % Identity 71.2
- Alignment Length 132
- Location of Alignment in SEQ ID NO 1251: from 4 to 128

- Alignment No. 9442
- gi No. 1763308
- % Identity 84.4
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9443
- gi No. 1870700
- % Identity 89.2
- Alignment Length 111
- Location of Alignment in SEQ ID NO 1251: from 1 to 111

- Alignment No. 9444
- gi No. 1881589
- % Identity 87.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1251: from 89 to 128

- Alignment No. 9445
- gi No. 1881594
- % Identity 91
- Alignment Length 89
- Location of Alignment in SEQ ID NO 1251: from 1 to 87

- Alignment No. 9446
- gi No. 1881601
- % Identity 93.1
- Alignment Length 87
- Location of Alignment in SEQ ID NO 1251: from 1 to 87

- Alignment No. 9447
- gi No. 19611
- % Identity 92.2
- Alignment Length 115
- Location of Alignment in SEQ ID NO 1251: from 14 to 128

- Alignment No. 9448
- gi No. 19614
- % Identity 90
- Alignment Length 50
- Location of Alignment in SEQ ID NO 1251: from 79 to 128

- Alignment No. 9449
- gi No. 208463
- % Identity 84.8
- Alignment Length 33
- Location of Alignment in SEQ ID NO 1251: from 3 to 35

- Alignment No. 9450
- gi No. 2116601
- % Identity 89.8
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9451
- gi No. 211855
- % Identity 90.6
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9452

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- gi No. 2119011
- % Identity 90.6
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9453
- gi No. 2119012
- % Identity 90.6
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9454
- gi No. 2119013
- % Identity 92.1
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1251: from 1 to 127

- Alignment No. 9455
- gi No. 2119014
- % Identity 91.2
- Alignment Length 68
- Location of Alignment in SEQ ID NO 1251: from 61 to 128

- Alignment No. 9456
- gi No. 2119018
- % Identity 91.4
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9457
- gi No. 2135356
- % Identity 88.9
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1251: from 1 to 27

- Alignment No. 9458
- gi No. 2136686
- % Identity 89.7
- Alignment Length 29
- Location of Alignment in SEQ ID NO 1251: from 2 to 30

- Alignment No. 9459
- gi No. 2147399
- % Identity 89.7
- Alignment Length 39
- Location of Alignment in SEQ ID NO 1251: from 1 to 39

- Alignment No. 9460
- gi No. 2252516
- % Identity 89.5
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1251: from 1 to 38

- Alignment No. 9461
- gi No. 2253166
- % Identity 87.3
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1251: from 1 to 63

- Alignment No. 9462
- gi No. 2253615

- % Identity 78.6
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9463
- gi No. 2909431
- % Identity 80.4
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1251: from 13 to 122

- Alignment No. 9464
- gi No. 2995216
- % Identity 77.8
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1251: from 1 to 36

- Alignment No. 9465
- gi No. 2995219
- % Identity 75
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1251: from 1 to 36

- Alignment No. 9466
- gi No. 2995225
- % Identity 83.3
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1251: from 1 to 36

- Alignment No. 9467
- gi No. 2995264
- % Identity 80.6
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1251: from 1 to 36

- Alignment No. 9468
- gi No. 3002595
- % Identity 90.1
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1251: from 15 to 105

- Alignment No. 9469
- gi No. 3002597
- % Identity 89
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1251: from 15 to 105

- Alignment No. 9470
- gi No. 3002603
- % Identity 87
- Alignment Length 92
- Location of Alignment in SEQ ID NO 1251: from 15 to 105

- Alignment No. 9471
- gi No. 3002613
- % Identity 87.9
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1251: from 15 to 105

- Alignment No. 9472
- gi No. 3002621
- % Identity 86.8

- Alignment Length 91
- Location of Alignment in SEQ ID NO 1251: from 15 to 105
- Alignment No. 9473
- gi No. 3002633
- % Identity 89
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1251: from 15 to 105
- Alignment No. 9474
- gi No. 3002635
- % Identity 89
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1251: from 15 to 105
- Alignment No. 9475
- gi No. 3002637
- % Identity 88.9
- Alignment Length 90
- Location of Alignment in SEQ ID NO 1251: from 16 to 105
- Alignment No. 9476
- gi No. 3002643
- % Identity 89
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1251: from 15 to 105
- Alignment No. 9477
- gi No. 3002647
- % Identity 90
- Alignment Length 90
- Location of Alignment in SEQ ID NO 1251: from 15 to 104
- Alignment No. 9478
- gi No. 3002649
- % Identity 87.6
- Alignment Length 89
- Location of Alignment in SEQ ID NO 1251: from 15 to 103
- Alignment No. 9479
- gi No. 3002657
- % Identity 89
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1251: from 15 to 105
- Alignment No. 9480
- gi No. 3002663
- % Identity 87.9
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1251: from 15 to 105
- Alignment No. 9481
- gi No. 3219788
- % Identity 84.8
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1251: from 13 to 122
- Alignment No. 9482
- gi No. 3219789
- % Identity 82.1
- Alignment Length 112

- Location of Alignment in SEQ ID NO 1251: from 13 to 122
- Alignment No. 9483
- gi No. 3219790
- % Identity 85.5
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1251: from 13 to 122
- Alignment No. 9484
- gi No. 3219791
- % Identity 83.9
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1251: from 13 to 122
- Alignment No. 9485
- gi No. 3219792
- % Identity 83.9
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1251: from 13 to 122
- Alignment No. 9486
- gi No. 3219803
- % Identity 81.3
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1251: from 13 to 122
- Alignment No. 9487
- gi No. 3219805
- % Identity 82.9
- Alignment Length 111
- Location of Alignment in SEQ ID NO 1251: from 13 to 122
- Alignment No. 9488
- gi No. 352175
- % Identity 83.5
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1251: from 2 to 128
- Alignment No. 9489
- gi No. 3745758
- % Identity 91.7
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1251: from 21 to 128
- Alignment No. 9490
- gi No. 386772
- % Identity 91.4
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
- Alignment No. 9491
- gi No. 3875420
- % Identity 82.8
- Alignment Length 116
- Location of Alignment in SEQ ID NO 1251: from 13 to 128
- Alignment No. 9492
- gi No. 3875421
- % Identity 76.4
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1251: from 1 to 127

- Alignment No. 9493
- gi No. 3880527
- % Identity 87.5
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9494
- gi No. 3880606
- % Identity 83.3
- Alignment Length 72
- Location of Alignment in SEQ ID NO 1251: from 57 to 128

- Alignment No. 9495
- gi No. 3979986
- % Identity 92.2
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9496
- gi No. 404466
- % Identity 89.8
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9497
- gi No. 4139869
- % Identity 90.6
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1251: from 44 to 128

- Alignment No. 9498
- gi No. 417103
- % Identity 95.3
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9499
- gi No. 422605
- % Identity 87.5
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9500
- gi No. 422606
- % Identity 90.6
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9501
- gi No. 4388695
- % Identity 89.7
- Alignment Length 68
- Location of Alignment in SEQ ID NO 1251: from 61 to 128

- Alignment No. 9502
- gi No. 4504279
- % Identity 91.4
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9503
- gi No. 4504281
- % Identity 91.4
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9504
- gi No. 4504283
- % Identity 90.6
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9505
- gi No. 4504299
- % Identity 88.3
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9506
- gi No. 4574208
- % Identity 97.2
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1251: from 22 to 128

- Alignment No. 9507
- gi No. 4761212
- % Identity 91.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1251: from 8 to 119

- Alignment No. 9508
- gi No. 484441
- % Identity 90.6
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9509
- gi No. 484530
- % Identity 90.6
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1251: from 2 to 128

- Alignment No. 9510
- gi No. 484531
- % Identity 90.6
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1251: from 2 to 128

- Alignment No. 9511
- gi No. 4883733
- % Identity 89.6
- Alignment Length 106
- Location of Alignment in SEQ ID NO 1251: from 11 to 116

- Alignment No. 9512
- gi No. 4883734
- % Identity 90.7
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1251: from 10 to 116

- Alignment No. 9513

- gi No. 4883735
- % Identity 90.8
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1251: from 9 to 117

- Alignment No. 9514
- gi No. 4883736
- % Identity 89.5
- Alignment Length 105
- Location of Alignment in SEQ ID NO 1251: from 11 to 115

- Alignment No. 9515
- gi No. 4883737
- % Identity 90.3
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1251: from 13 to 115

- Alignment No. 9516
- gi No. 4883738
- % Identity 87.1
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1251: from 17 to 109

- Alignment No. 9517
- gi No. 4883739
- % Identity 90.4
- Alignment Length 104
- Location of Alignment in SEQ ID NO 1251: from 13 to 116

- Alignment No. 9518
- gi No. 4883740
- % Identity 89.3
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1251: from 13 to 115

- Alignment No. 9519
- gi No. 4883741
- % Identity 90.7
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1251: from 9 to 116

- Alignment No. 9520
- gi No. 4883743
- % Identity 88.1
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1251: from 9 to 117

- Alignment No. 9521
- gi No. 4883744
- % Identity 89.9
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1251: from 9 to 117

- Alignment No. 9522
- gi No. 4883745
- % Identity 90.7
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1251: from 9 to 116

- Alignment No. 9523
- gi No. 4883746

- % Identity 88.9
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1251: from 9 to 116

- Alignment No. 9524
- gi No. 4883747
- % Identity 89.9
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1251: from 9 to 117

- Alignment No. 9525
- gi No. 4883748
- % Identity 89.9
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1251: from 9 to 117

- Alignment No. 9526
- gi No. 4883749
- % Identity 91.4
- Alignment Length 105
- Location of Alignment in SEQ ID NO 1251: from 13 to 117

- Alignment No. 9527
- gi No. 4883751
- % Identity 89.8
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1251: from 9 to 116

- Alignment No. 9528
- gi No. 4883752
- % Identity 89.8
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1251: from 10 to 117

- Alignment No. 9529
- gi No. 4883753
- % Identity 89.9
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1251: from 9 to 117

- Alignment No. 9530
- gi No. 4883754
- % Identity 88.8
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1251: from 9 to 115

- Alignment No. 9531
- gi No. 4883755
- % Identity 91.3
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1251: from 13 to 115

- Alignment No. 9532
- gi No. 4883756
- % Identity 89.9
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1251: from 9 to 117

- Alignment No. 9533
- gi No. 4883758
- % Identity 91.2

- Alignment Length 102
- Location of Alignment in SEQ ID NO 1251: from 13 to 114
- Alignment No. 9534
- gi No. 4883759
- % Identity 89
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1251: from 9 to 117
- Alignment No. 9535
- gi No. 4883760
- % Identity 88.1
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1251: from 9 to 117
- Alignment No. 9536
- gi No. 4883762
- % Identity 88.9
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1251: from 9 to 116
- Alignment No. 9537
- gi No. 488571
- % Identity 95
- Alignment Length 119
- Location of Alignment in SEQ ID NO 1251: from 10 to 128
- Alignment No. 9538
- gi No. 488573
- % Identity 95.7
- Alignment Length 116
- Location of Alignment in SEQ ID NO 1251: from 13 to 128
- Alignment No. 9539
- gi No. 529954
- % Identity 82.6
- Alignment Length 132
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
- Alignment No. 9540
- gi No. 539427
- % Identity 91.7
- Alignment Length 48
- Location of Alignment in SEQ ID NO 1251: from 2 to 49
- Alignment No. 9541
- gi No. 556612
- % Identity 84.4
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
- Alignment No. 9542
- gi No. 559807
- % Identity 89.1
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
- Alignment No. 9543
- gi No. 578470
- % Identity 88.2
- Alignment Length 68

- Location of Alignment in SEQ ID NO 1251: from 61 to 128
- Alignment No. 9544
- gi No. 630475
- % Identity 85.5
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1251: from 1 to 76
- Alignment No. 9545
- gi No. 630476
- % Identity 85.7
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1251: from 1 to 63
- Alignment No. 9546
- gi No. 631693
- % Identity 88
- Alignment Length 50
- Location of Alignment in SEQ ID NO 1251: from 79 to 128
- Alignment No. 9547
- gi No. 70743
- % Identity 91.3
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1251: from 2 to 128
- Alignment No. 9548
- gi No. 70747
- % Identity 90.6
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1251: from 2 to 128
- Alignment No. 9549
- gi No. 70748
- % Identity 89.8
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1251: from 2 to 128
- Alignment No. 9550
- gi No. 70749
- % Identity 91.3
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1251: from 2 to 128
- Alignment No. 9551
- gi No. 70753
- % Identity 92.1
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1251: from 2 to 128
- Alignment No. 9552
- gi No. 70755
- % Identity 87.4
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1251: from 2 to 128
- Alignment No. 9553
- gi No. 70760
- % Identity 77.1
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1251: from 2 to 132

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- Alignment No. 9554
- gi No. 729676
- % Identity 84.4
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9555
- gi No. 729677
- % Identity 82.8
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9556
- gi No. 81850
- % Identity 95.5
- Alignment Length 111
- Location of Alignment in SEQ ID NO 1251: from 18 to 128

- Alignment No. 9557
- gi No. 84300
- % Identity 80.5
- Alignment Length 41
- Location of Alignment in SEQ ID NO 1251: from 1 to 41

- Alignment No. 9558
- gi No. 84329
- % Identity 84.3
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1251: from 2 to 128

- Alignment No. 9559
- gi No. 85000
- % Identity 91.3
- Alignment Length 115
- Location of Alignment in SEQ ID NO 1251: from 2 to 116

- Alignment No. 9560
- gi No. 85001
- % Identity 89.8
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9561
- gi No. 90622
- % Identity 90.6
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9562
- gi No. 995959
- % Identity 82.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1251: from 1 to 40

- Alignment No. 9563
- gi No. 99980
- % Identity 90.6
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1251: from 85 to 116

- Alignment No. 9564
- gi No. 99980
- % Identity 88.6
- Alignment Length 44
- Location of Alignment in SEQ ID NO 1251: from 2 to 45

- Alignment No. 9565
- gi No. 99981
- % Identity 78.1
- Alignment Length 64
- Location of Alignment in SEQ ID NO 1251: from 2 to 65

Maximum Length Sequence corresponding to clone ID 253173

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1252
- Ceres seq_id 1499960

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1253
- Ceres seq_id 1499961
- Location of start within SEQ ID NO 1252: at 121 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9566
- O-methyltransferase
- Location within SEQ ID NO 1253: from 97 to 338 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9567
- gi No. 1169009
- % Identity 76.6
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1253: from 1 to 361

- Alignment No. 9568
- gi No. 116908
- % Identity 77
- Alignment Length 365
- Location of Alignment in SEQ ID NO 1253: from 1 to 363

- Alignment No. 9569
- gi No. 1184041
- % Identity 78.4
- Alignment Length 343
- Location of Alignment in SEQ ID NO 1253: from 21 to 363

- Alignment No. 9570
- gi No. 1236980
- % Identity 74.4
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1253: from 1 to 362

- Alignment No. 9571
- gi No. 1582580
- % Identity 73.9
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1253: from 1 to 362

- Alignment No. 9572
- gi No. 170277
- % Identity 81.6

- Alignment Length 114
- Location of Alignment in SEQ ID NO 1253: from 231 to 344

- Alignment No. 9573
- gi No. 1791352
- % Identity 76.5
- Alignment Length 349
- Location of Alignment in SEQ ID NO 1253: from 15 to 361

- Alignment No. 9574
- gi No. 231757
- % Identity 79.4
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1253: from 1 to 362

- Alignment No. 9575
- gi No. 252735
- % Identity 90
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1253: from 163 to 182

- Alignment No. 9576
- gi No. 2781394
- % Identity 99.7
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1253: from 1 to 363

- Alignment No. 9577
- gi No. 3421382
- % Identity 71.5
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1253: from 1 to 361

- Alignment No. 9578
- gi No. 3913289
- % Identity 77.2
- Alignment Length 368
- Location of Alignment in SEQ ID NO 1253: from 1 to 361

- Alignment No. 9579
- gi No. 3913295
- % Identity 79.7
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1253: from 1 to 362

- Alignment No. 9580
- gi No. 444327
- % Identity 78.8
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1253: from 1 to 361

- Alignment No. 9581
- gi No. 4468044
- % Identity 77.1
- Alignment Length 140
- Location of Alignment in SEQ ID NO 1253: from 222 to 361

- Alignment No. 9582
- gi No. 4468046
- % Identity 76.4
- Alignment Length 365

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- Location of Alignment in SEQ ID NO 1253: from 1 to 363
- Alignment No. 9583
- gi No. 4468048
- % Identity 74.1
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1253: from 1 to 361
- Alignment No. 9584
- gi No. 4468050
- % Identity 80.1
- Alignment Length 226
- Location of Alignment in SEQ ID NO 1253: from 136 to 361
- Alignment No. 9585
- gi No. 480082
- % Identity 77.5
- Alignment Length 346
- Location of Alignment in SEQ ID NO 1253: from 1 to 344
- Alignment No. 9586
- gi No. 480083
- % Identity 76.9
- Alignment Length 346
- Location of Alignment in SEQ ID NO 1253: from 1 to 344
- Alignment No. 9587
- gi No. 4808522
- % Identity 70.6
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1253: from 1 to 361
- Alignment No. 9588
- gi No. 4808524
- % Identity 71.8
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1253: from 1 to 361
- Alignment No. 9589
- gi No. 4808526
- % Identity 71.5
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1253: from 1 to 361
- Alignment No. 9590
- gi No. 4808528
- % Identity 70.6
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1253: from 1 to 361
- Alignment No. 9591
- gi No. 4808530
- % Identity 72.1
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1253: from 1 to 361
- Alignment No. 9592
- gi No. 5031492
- % Identity 74.8
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1253: from 1 to 361

- Alignment No. 9593
- gi No. 5031494
- % Identity 75.1
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1253: from 1 to 361

- Alignment No. 9594
- gi No. 642952
- % Identity 70.2
- Alignment Length 350
- Location of Alignment in SEQ ID NO 1253: from 16 to 361

- Alignment No. 9595
- gi No. 762870
- % Identity 78.6
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1253: from 1 to 362

- Alignment No. 9596
- gi No. 762872
- % Identity 74.7
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1253: from 1 to 362

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1254
- Ceres seq_id 1499962
- Location of start within SEQ ID NO 1252: at 190 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9597
- O-methyltransferase
- Location within SEQ ID NO 1254: from 74 to 315 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9598
- gi No. 1169009
- % Identity 76.6
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1254: from 1 to 338

- Alignment No. 9599
- gi No. 116908
- % Identity 77
- Alignment Length 365
- Location of Alignment in SEQ ID NO 1254: from 1 to 340

- Alignment No. 9600
- gi No. 1184041
- % Identity 78.4
- Alignment Length 343
- Location of Alignment in SEQ ID NO 1254: from 1 to 340

- Alignment No. 9601
- gi No. 1236980
- % Identity 74.4
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1254: from 1 to 339

- Alignment No. 9602
- gi No. 1582580
- % Identity 73.9
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1254: from 1 to 339

- Alignment No. 9603
- gi No. 170277
- % Identity 81.6
- Alignment Length 114
- Location of Alignment in SEQ ID NO 1254: from 208 to 321

- Alignment No. 9604
- gi No. 1791352
- % Identity 76.5
- Alignment Length 349
- Location of Alignment in SEQ ID NO 1254: from 1 to 338

- Alignment No. 9605
- gi No. 231757
- % Identity 79.4
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1254: from 1 to 339

- Alignment No. 9606
- gi No. 252735
- % Identity 90
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1254: from 140 to 159

- Alignment No. 9607
- gi No. 2781394
- % Identity 99.7
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1254: from 1 to 340

- Alignment No. 9608
- gi No. 3421382
- % Identity 71.5
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1254: from 1 to 338

- Alignment No. 9609
- gi No. 3913289
- % Identity 77.2
- Alignment Length 368
- Location of Alignment in SEQ ID NO 1254: from 1 to 338

- Alignment No. 9610
- gi No. 3913295
- % Identity 79.7
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1254: from 1 to 339

- Alignment No. 9611
- gi No. 444327
- % Identity 78.8
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1254: from 1 to 338

- Alignment No. 9612

- ```
- gi No. 4468044
- % Identity 77.1
- Alignment Length 140
- Location of Alignment in SEQ ID NO 1254: from 199 to 338

- Alignment No. 9613
- gi No. 4468046
- % Identity 76.4
- Alignment Length 365
- Location of Alignment in SEQ ID NO 1254: from 1 to 340

- Alignment No. 9614
- gi No. 4468048
- % Identity 74.1
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1254: from 1 to 338

- Alignment No. 9615
- gi No. 4468050
- % Identity 80.1
- Alignment Length 226
- Location of Alignment in SEQ ID NO 1254: from 113 to 338

- Alignment No. 9616
- gi No. 480082
- % Identity 77.5
- Alignment Length 346
- Location of Alignment in SEQ ID NO 1254: from 1 to 321

- Alignment No. 9617
- gi No. 480083
- % Identity 76.9
- Alignment Length 346
- Location of Alignment in SEQ ID NO 1254: from 1 to 321

- Alignment No. 9618
- gi No. 4808522
- % Identity 70.6
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1254: from 1 to 338

- Alignment No. 9619
- gi No. 4808524
- % Identity 71.8
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1254: from 1 to 338

- Alignment No. 9620
- gi No. 4808526
- % Identity 71.5
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1254: from 1 to 338

- Alignment No. 9621
- gi No. 4808528
- % Identity 70.6
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1254: from 1 to 338

- Alignment No. 9622
- gi No. 4808530
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- % Identity 72.1
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1254: from 1 to 338
  
- Alignment No. 9623
- gi No. 5031492
- % Identity 74.8
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1254: from 1 to 338
  
- Alignment No. 9624
- gi No. 5031494
- % Identity 75.1
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1254: from 1 to 338
  
- Alignment No. 9625
- gi No. 642952
- % Identity 70.2
- Alignment Length 350
- Location of Alignment in SEQ ID NO 1254: from 1 to 338
  
- Alignment No. 9626
- gi No. 762870
- % Identity 78.6
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1254: from 1 to 339
  
- Alignment No. 9627
- gi No. 762872
- % Identity 74.7
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1254: from 1 to 339

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1255
- Ceres seq\_id 1499963
- Location of start within SEQ ID NO 1252: at 220 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9628
- O-methyltransferase
- Location within SEQ ID NO 1255: from 64 to 305 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9629
- gi No. 1169009
- % Identity 76.6
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1255: from 1 to 328
  
- Alignment No. 9630
- gi No. 116908
- % Identity 77
- Alignment Length 365
- Location of Alignment in SEQ ID NO 1255: from 1 to 330
  
- Alignment No. 9631
- gi No. 1184041
- % Identity 78.4

- Alignment Length 343
- Location of Alignment in SEQ ID NO 1255: from 1 to 330
- Alignment No. 9632
- gi No. 1236980
- % Identity 74.4
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1255: from 1 to 329
- Alignment No. 9633
- gi No. 1582580
- % Identity 73.9
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1255: from 1 to 329
- Alignment No. 9634
- gi No. 170277
- % Identity 81.6
- Alignment Length 114
- Location of Alignment in SEQ ID NO 1255: from 198 to 311
- Alignment No. 9635
- gi No. 1791352
- % Identity 76.5
- Alignment Length 349
- Location of Alignment in SEQ ID NO 1255: from 1 to 328
- Alignment No. 9636
- gi No. 231757
- % Identity 79.4
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1255: from 1 to 329
- Alignment No. 9637
- gi No. 252735
- % Identity 90
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1255: from 130 to 149
- Alignment No. 9638
- gi No. 2781394
- % Identity 99.7
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1255: from 1 to 330
- Alignment No. 9639
- gi No. 3421382
- % Identity 71.5
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1255: from 1 to 328
- Alignment No. 9640
- gi No. 3913289
- % Identity 77.2
- Alignment Length 368
- Location of Alignment in SEQ ID NO 1255: from 1 to 328
- Alignment No. 9641
- gi No. 3913295
- % Identity 79.7
- Alignment Length 364

- Location of Alignment in SEQ ID NO 1255: from 1 to 329
- Alignment No. 9642
- gi No. 444327
- % Identity 78.8
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1255: from 1 to 328
- Alignment No. 9643
- gi No. 4468044
- % Identity 77.1
- Alignment Length 140
- Location of Alignment in SEQ ID NO 1255: from 189 to 328
- Alignment No. 9644
- gi No. 4468046
- % Identity 76.4
- Alignment Length 365
- Location of Alignment in SEQ ID NO 1255: from 1 to 330
- Alignment No. 9645
- gi No. 4468048
- % Identity 74.1
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1255: from 1 to 328
- Alignment No. 9646
- gi No. 4468050
- % Identity 80.1
- Alignment Length 226
- Location of Alignment in SEQ ID NO 1255: from 103 to 328
- Alignment No. 9647
- gi No. 480082
- % Identity 77.5
- Alignment Length 346
- Location of Alignment in SEQ ID NO 1255: from 1 to 311
- Alignment No. 9648
- gi No. 480083
- % Identity 76.9
- Alignment Length 346
- Location of Alignment in SEQ ID NO 1255: from 1 to 311
- Alignment No. 9649
- gi No. 4808522
- % Identity 70.6
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1255: from 1 to 328
- Alignment No. 9650
- gi No. 4808524
- % Identity 71.8
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1255: from 1 to 328
- Alignment No. 9651
- gi No. 4808526
- % Identity 71.5
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1255: from 1 to 328

- Alignment No. 9652
- gi No. 4808528
- % Identity 70.6
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1255: from 1 to 328
  
- Alignment No. 9653
- gi No. 4808530
- % Identity 72.1
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1255: from 1 to 328
  
- Alignment No. 9654
- gi No. 5031492
- % Identity 74.8
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1255: from 1 to 328
  
- Alignment No. 9655
- gi No. 5031494
- % Identity 75.1
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1255: from 1 to 328
  
- Alignment No. 9656
- gi No. 642952
- % Identity 70.2
- Alignment Length 350
- Location of Alignment in SEQ ID NO 1255: from 1 to 328
  
- Alignment No. 9657
- gi No. 762870
- % Identity 78.6
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1255: from 1 to 329
  
- Alignment No. 9658
- gi No. 762872
- % Identity 74.7
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1255: from 1 to 329

Maximum Length Sequence corresponding to clone ID 253258

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1256
- Ceres seq\_id 1499964

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1257
- Ceres seq\_id 1499965
- Location of start within SEQ ID NO 1256: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9659
- gi No. 3785990
- % Identity 84.7
- Alignment Length 157
- Location of Alignment in SEQ ID NO 1257: from 15 to 99

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1258
  - Ceres seq\_id 1499966
  - Location of start within SEQ ID NO 1256: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1259
  - Ceres seq\_id 1499967
  - Location of start within SEQ ID NO 1256: at 434 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
  - Alignment No. 9660
  - gi No. 3785990
  - % Identity 98.9
  - Alignment Length 95
  - Location of Alignment in SEQ ID NO 1259: from 1 to 92

Maximum Length Sequence corresponding to clone ID 253262

- (A) Polynucleotide Sequence
  - Pat. Appln. SEQ ID NO 1260
  - Ceres seq\_id 1499968
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1261
  - Ceres seq\_id 1499969
  - Location of start within SEQ ID NO 1260: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
  - Alignment No. 9661
  - gi No. 3152605
  - % Identity 98.8
  - Alignment Length 83
  - Location of Alignment in SEQ ID NO 1261: from 4 to 84
- Alignment No. 9662
  - gi No. 4006889
  - % Identity 83.1
  - Alignment Length 83
  - Location of Alignment in SEQ ID NO 1261: from 4 to 84

Maximum Length Sequence corresponding to clone ID 253359

- (A) Polynucleotide Sequence
  - Pat. Appln. SEQ ID NO 1262
  - Ceres seq\_id 1499970
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1263
  - Ceres seq\_id 1499971
  - Location of start within SEQ ID NO 1262: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9663
- Hsp90 protein
- Location within SEQ ID NO 1263: from 36 to 110 aa.

- Alignment No. 9664
- Hsp90 protein
- Location within SEQ ID NO 1263: from 39 to 138 aa.
  
- Alignment No. 9665
- Hsp90 protein
- Location within SEQ ID NO 1263: from 131 to 181 aa.
  
- Alignment No. 9666
- 11-S plant seed storage protein
- Location within SEQ ID NO 1263: from 14 to 95 aa.
  
- Alignment No. 9667
- Troponin
- Location within SEQ ID NO 1263: from 25 to 123 aa.
  
- Alignment No. 9668
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 1263: from 7 to 85 aa.
  
- Alignment No. 9669
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 1263: from 7 to 88 aa.
  
- Alignment No. 9670
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 1263: from 9 to 86 aa.
  
- Alignment No. 9671
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 1263: from 17 to 133 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 253404

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1264
- Ceres seq\_id 1499972

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1265
- Ceres seq\_id 1499973
- Location of start within SEQ ID NO 1264: at 131 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9672
- Glycosyl hydrolase family 9
- Location within SEQ ID NO 1265: from 58 to 514 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1266
- Ceres seq\_id 1499974
- Location of start within SEQ ID NO 1264: at 479 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9673
- Glycosyl hydrolase family 9

- Location within SEQ ID NO 1266: from 1 to 398 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1267
- Ceres seq\_id 1499975
- Location of start within SEQ ID NO 1264: at 533 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9674
- Glycosyl hydrolase family 9
- Location within SEQ ID NO 1267: from 1 to 380 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 253420

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1268
- Ceres seq\_id 1499976

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1269
- Ceres seq\_id 1499977
- Location of start within SEQ ID NO 1268: at 159 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9675
- gi No. 3928150
- % Identity 78.6
- Alignment Length 28
- Location of Alignment in SEQ ID NO 1269: from 1 to 28

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1270
- Ceres seq\_id 1499978
- Location of start within SEQ ID NO 1268: at 563 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1271
- Ceres seq\_id 1499979
- Location of start within SEQ ID NO 1268: at 638 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 253499

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1272
- Ceres seq\_id 1499984

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1273
- Ceres seq\_id 1499985
- Location of start within SEQ ID NO 1272: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9676
- alpha/beta hydrolase fold
- Location within SEQ ID NO 1273: from 96 to 318 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1274
- Ceres seq\_id 1499986
- Location of start within SEQ ID NO 1272: at 30 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9677
- alpha/beta hydrolase fold
- Location within SEQ ID NO 1274: from 87 to 309 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 253505

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1275
- Ceres seq\_id 1499989

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1276
- Ceres seq\_id 1499990
- Location of start within SEQ ID NO 1275: at 206 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9678
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1276: from 83 to 360 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9679
- gi No. 2351097
- % Identity 99.5
- Alignment Length 391
- Location of Alignment in SEQ ID NO 1276: from 1 to 391

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1277
- Ceres seq\_id 1499991
- Location of start within SEQ ID NO 1275: at 356 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9680
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1277: from 33 to 310 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9681
- gi No. 2351097
- % Identity 99.5
- Alignment Length 391
- Location of Alignment in SEQ ID NO 1277: from 1 to 341



- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1278
  - Ceres seq\_id 1499992
  - Location of start within SEQ ID NO 1275: at 422 nt.

- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
  - Alignment No. 9682
  - Eukaryotic protein kinase domain
  - Location within SEQ ID NO 1278: from 11 to 288 aa.

- (D) Related Amino Acid Sequences
  - Alignment No. 9683
  - gi No. 2351097
  - % Identity 99.5
  - Alignment Length 391
  - Location of Alignment in SEQ ID NO 1278: from 1 to 319

Maximum Length Sequence corresponding to clone ID 253633

- (A) Polynucleotide Sequence
  - Pat. Appln. SEQ ID NO 1279
  - Ceres seq\_id 1499993
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1280
  - Ceres seq\_id 1499994
  - Location of start within SEQ ID NO 1279: at 198 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
  - Alignment No. 9684
  - Eukaryotic protein kinase domain
  - Location within SEQ ID NO 1280: from 3 to 125 aa.

- (D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 253648

- (A) Polynucleotide Sequence
  - Pat. Appln. SEQ ID NO 1281
  - Ceres seq\_id 1499995
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1282
  - Ceres seq\_id 1499996
  - Location of start within SEQ ID NO 1281: at 1 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
- (D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1283
  - Ceres seq\_id 1499997
  - Location of start within SEQ ID NO 1281: at 60 nt.

- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
- (D) Related Amino Acid Sequences
  - Alignment No. 9685
  - gi No. 1209262
  - % Identity 71
  - Alignment Length 63

- Location of Alignment in SEQ ID NO 1283: from 5 to 66
- Alignment No. 9686
- gi No. 125408
- % Identity 92.4
- Alignment Length 66
- Location of Alignment in SEQ ID NO 1283: from 1 to 66
- Alignment No. 9687
- gi No. 167146
- % Identity 71
- Alignment Length 62
- Location of Alignment in SEQ ID NO 1283: from 5 to 66
- Alignment No. 9688
- gi No. 399298
- % Identity 100
- Alignment Length 66
- Location of Alignment in SEQ ID NO 1283: from 1 to 66
- Alignment No. 9689
- gi No. 4493273
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1283: from 27 to 63
- Alignment No. 9690
- gi No. 4493276
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1283: from 27 to 63
- Alignment No. 9691
- gi No. 4494076
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1283: from 27 to 63
- Alignment No. 9692
- gi No. 4538893
- % Identity 91.9
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1283: from 27 to 63

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1284
- Ceres seq\_id 1499998
- Location of start within SEQ ID NO 1281: at 79 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 253653

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1285
- Ceres seq\_id 1499999

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1286
- Ceres seq\_id 1500000
- Location of start within SEQ ID NO 1285: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9693
- Plant lipid transfer protein family
- Location within SEQ ID NO 1286: from 45 to 76 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1287
- Ceres seq\_id 1500001
- Location of start within SEQ ID NO 1285: at 37 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9694
- Plant lipid transfer protein family
- Location within SEQ ID NO 1287: from 33 to 64 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1288
- Ceres seq\_id 1500002
- Location of start within SEQ ID NO 1285: at 85 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9695
- Plant lipid transfer protein family
- Location within SEQ ID NO 1288: from 17 to 48 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 253679

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1289
- Ceres seq\_id 1500003

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1290
- Ceres seq\_id 1500004
- Location of start within SEQ ID NO 1289: at 603 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9696
- gi No. 4455227
- % Identity 100
- Alignment Length 178
- Location of Alignment in SEQ ID NO 1290: from 37 to 214

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1291
- Ceres seq\_id 1500005
- Location of start within SEQ ID NO 1289: at 606 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9697
- gi No. 4455227
- % Identity 100
- Alignment Length 178
- Location of Alignment in SEQ ID NO 1291: from 36 to 213

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1292
- Ceres seq\_id 1500006
- Location of start within SEQ ID NO 1289: at 711 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9698
- gi No. 4455227
- % Identity 100
- Alignment Length 178
- Location of Alignment in SEQ ID NO 1292: from 1 to 178

Maximum Length Sequence corresponding to clone ID 253698

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1293
- Ceres seq\_id 1500007

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1294
- Ceres seq\_id 1500008
- Location of start within SEQ ID NO 1293: at 20 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9699
- Cytochrome P450
- Location within SEQ ID NO 1294: from 31 to 481 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9700
- gi No. 4006850
- % Identity 83.3
- Alignment Length 180
- Location of Alignment in SEQ ID NO 1294: from 314 to 492
  
- Alignment No. 9701
- gi No. 4006851
- % Identity 73.8
- Alignment Length 500
- Location of Alignment in SEQ ID NO 1294: from 1 to 494
  
- Alignment No. 9702
- gi No. 4468802
- % Identity 76.1
- Alignment Length 494
- Location of Alignment in SEQ ID NO 1294: from 1 to 492
  
- Alignment No. 9703
- gi No. 4468803
- % Identity 98.8
- Alignment Length 494
- Location of Alignment in SEQ ID NO 1294: from 1 to 494

(B) Polypeptide Sequence

- ```
- Pat. Appln. SEQ ID NO 1295
- Ceres seq_id 1500009
- Location of start within SEQ ID NO 1293: at 365 nt.
```

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9704
- Cytochrome P450
- Location within SEQ ID NO 1295: from 1 to 366 aa.

(D) Related Amino Acid Sequences

- ```
- Alignment No. 9705
- gi No. 4006850
- % Identity 83.3
- Alignment Length 180
- Location of Alignment in SEQ ID NO 1295: from 199 to 377

- Alignment No. 9706
- gi No. 4006851
- % Identity 73.8
- Alignment Length 500
- Location of Alignment in SEQ ID NO 1295: from 1 to 379

- Alignment No. 9707
- gi No. 4468802
- % Identity 76.1
- Alignment Length 494
- Location of Alignment in SEQ ID NO 1295: from 1 to 377

- Alignment No. 9708
- gi No. 4468803
- % Identity 98.8
- Alignment Length 494
- Location of Alignment in SEQ ID NO 1295: from 1 to 379
```

(B) Polypeptide Sequence

- ```
- Pat. Appln. SEQ ID NO 1296
- Ceres seq_id 1500010
- Location of start within SEQ ID NO 1293: at 536 nt.
```

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9709
- Cytochrome P450
- Location within SEQ ID NO 1296: from 1 to 309 aa.

(D) Related Amino Acid Sequences

- ```
- Alignment No. 9710
- gi No. 4006850
- % Identity 83.3
- Alignment Length 180
- Location of Alignment in SEQ ID NO 1296: from 142 to 320

- Alignment No. 9711
- gi No. 4006851
- % Identity 73.8
- Alignment Length 500
- Location of Alignment in SEQ ID NO 1296: from 1 to 322

- Alignment No. 9712
- gi No. 4468802
```

- % Identity 76.1
- Alignment Length 494
- Location of Alignment in SEQ ID NO 1296: from 1 to 320
- Alignment No. 9713
- gi No. 4468803
- % Identity 98.8
- Alignment Length 494
- Location of Alignment in SEQ ID NO 1296: from 1 to 322

Maximum Length Sequence corresponding to clone ID 253770

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1297
- Ceres seq\_id 1500011

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1298
- Ceres seq\_id 1500012
- Location of start within SEQ ID NO 1297: at 95 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9714
- Inositol monophosphatase family
- Location within SEQ ID NO 1298: from 122 to 327 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9715
- gi No. 1354510
- % Identity 100
- Alignment Length 373
- Location of Alignment in SEQ ID NO 1298: from 1 to 373
- Alignment No. 9716
- gi No. 2736075
- % Identity 99.5
- Alignment Length 373
- Location of Alignment in SEQ ID NO 1298: from 1 to 373

Maximum Length Sequence corresponding to clone ID 253849

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1299
- Ceres seq\_id 1500017

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1300
- Ceres seq\_id 1500018
- Location of start within SEQ ID NO 1299: at 106 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9717
- Zinc finger, C3HC4 type (RING finger)
- Location within SEQ ID NO 1300: from 201 to 241 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9718
- gi No. 2642154
- % Identity 96.3
- Alignment Length 354
- Location of Alignment in SEQ ID NO 1300: from 1 to 354

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1301
- Ceres seq\_id 1500019
- Location of start within SEQ ID NO 1299: at 325 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9719
- Zinc finger, C3HC4 type (RING finger)
- Location within SEQ ID NO 1301: from 128 to 168 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9720
- gi No. 2642154
- % Identity 96.3
- Alignment Length 354
- Location of Alignment in SEQ ID NO 1301: from 1 to 281

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1302
- Ceres seq\_id 1500020
- Location of start within SEQ ID NO 1299: at 472 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9721
- Zinc finger, C3HC4 type (RING finger)
- Location within SEQ ID NO 1302: from 79 to 119 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9722
- gi No. 2642154
- % Identity 96.3
- Alignment Length 354
- Location of Alignment in SEQ ID NO 1302: from 1 to 232

Maximum Length Sequence corresponding to clone ID 254111

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1303
- Ceres seq\_id 1500025

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1304
- Ceres seq\_id 1500026
- Location of start within SEQ ID NO 1303: at 381 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9723
- gi No. 5541682
- % Identity 98.7
- Alignment Length 157
- Location of Alignment in SEQ ID NO 1304: from 18 to 174

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1305
- Ceres seq\_id 1500027
- Location of start within SEQ ID NO 1303: at 522 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9724
- gi No. 5541682
- % Identity 98.7
- Alignment Length 157
- Location of Alignment in SEQ ID NO 1305: from 1 to 127

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1306
- Ceres seq\_id 1500028
- Location of start within SEQ ID NO 1303: at 528 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9725
- gi No. 5541682
- % Identity 98.7
- Alignment Length 157
- Location of Alignment in SEQ ID NO 1306: from 1 to 125

Maximum Length Sequence corresponding to clone ID 254513

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1307
- Ceres seq\_id 1500036

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1308
- Ceres seq\_id 1500037
- Location of start within SEQ ID NO 1307: at 613 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9726
- gi No. 4006920
- % Identity 99.3
- Alignment Length 400
- Location of Alignment in SEQ ID NO 1308: from 1 to 373

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1309
- Ceres seq\_id 1500038
- Location of start within SEQ ID NO 1307: at 718 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9727
- gi No. 4006920
- % Identity 99.3
- Alignment Length 400
- Location of Alignment in SEQ ID NO 1309: from 1 to 338

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1310
- Ceres seq\_id 1500039
- Location of start within SEQ ID NO 1307: at 868 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9728



- gi No. 4006920
- % Identity 99.3
- Alignment Length 400
- Location of Alignment in SEQ ID NO 1310: from 1 to 288

Maximum Length Sequence corresponding to clone ID 254633

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1311
- Ceres seq\_id 1500040

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1312
- Ceres seq\_id 1500041
- Location of start within SEQ ID NO 1311: at 98 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9729
- gi No. 2935529
- % Identity 76
- Alignment Length 217
- Location of Alignment in SEQ ID NO 1312: from 101 to 317
  
- Alignment No. 9730
- gi No. 3687238
- % Identity 100
- Alignment Length 234
- Location of Alignment in SEQ ID NO 1312: from 76 to 309
  
- Alignment No. 9731
- gi No. 4539422
- % Identity 73.9
- Alignment Length 319
- Location of Alignment in SEQ ID NO 1312: from 1 to 317

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1313
- Ceres seq\_id 1500042
- Location of start within SEQ ID NO 1311: at 242 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9732
- gi No. 2935529
- % Identity 76
- Alignment Length 217
- Location of Alignment in SEQ ID NO 1313: from 53 to 269
  
- Alignment No. 9733
- gi No. 3687238
- % Identity 100
- Alignment Length 234
- Location of Alignment in SEQ ID NO 1313: from 28 to 261
  
- Alignment No. 9734
- gi No. 4539422
- % Identity 73.9
- Alignment Length 319
- Location of Alignment in SEQ ID NO 1313: from 1 to 269

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1314
- Ceres seq\_id 1500043
- Location of start within SEQ ID NO 1311: at 323 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9735
- gi No. 2935529
- % Identity 76
- Alignment Length 217
- Location of Alignment in SEQ ID NO 1314: from 26 to 242
- Alignment No. 9736
- gi No. 3687238
- % Identity 100
- Alignment Length 234
- Location of Alignment in SEQ ID NO 1314: from 1 to 234
- Alignment No. 9737
- gi No. 4539422
- % Identity 73.9
- Alignment Length 319
- Location of Alignment in SEQ ID NO 1314: from 1 to 242

Maximum Length Sequence corresponding to clone ID 254758

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1315
- Ceres seq\_id 1500050

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1316
- Ceres seq\_id 1500051
- Location of start within SEQ ID NO 1315: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9738
- TBC domain
- Location within SEQ ID NO 1316: from 156 to 275 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9739
- gi No. 2880048
- % Identity 96.9
- Alignment Length 254
- Location of Alignment in SEQ ID NO 1316: from 143 to 275

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1317
- Ceres seq\_id 1500052
- Location of start within SEQ ID NO 1315: at 51 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9740
- TBC domain
- Location within SEQ ID NO 1317: from 140 to 259 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9741

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- gi No. 2880048
- % Identity 96.9
- Alignment Length 254
- Location of Alignment in SEQ ID NO 1317: from 127 to 259

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1318
- Ceres seq\_id 1500053
- Location of start within SEQ ID NO 1315: at 408 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9742
- TBC domain
- Location within SEQ ID NO 1318: from 21 to 140 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9743
- gi No. 2880048
- % Identity 96.9
- Alignment Length 254
- Location of Alignment in SEQ ID NO 1318: from 8 to 140

Maximum Length Sequence corresponding to clone ID 254801

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1319
- Ceres seq\_id 1500054

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1320
- Ceres seq\_id 1500055
- Location of start within SEQ ID NO 1319: at 401 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9744
- Ubiquitin family
- Location within SEQ ID NO 1320: from 1 to 76 aa.

- Alignment No. 9745
- Ubiquitin family
- Location within SEQ ID NO 1320: from 77 to 146 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9746
- gi No. 100490
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 9747
- gi No. 100490
- % Identity 100
- Alignment Length 137
- Location of Alignment in SEQ ID NO 1320: from 10 to 146
- Alignment No. 9748
- gi No. 100490
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9749
- gi No. 100490
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9750
- gi No. 100524
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9751
- gi No. 100524
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9752
- gi No. 100524
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9753
- gi No. 100524
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9754
- gi No. 100524
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9755
- gi No. 100524
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9756
- gi No. 100525
- % Identity 100
- Alignment Length 106
- Location of Alignment in SEQ ID NO 1320: from 1 to 106
  
- Alignment No. 9757
- gi No. 100525
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9758
- gi No. 100525
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9759

- gi No. 100525
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9760
- gi No. 100598
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9761
- gi No. 100598
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9762
- gi No. 100599
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9763
- gi No. 100599
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9764
- gi No. 100812
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9765
- gi No. 100812
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9766
- gi No. 100934
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9767
- gi No. 100934
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9768
- gi No. 100934
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9769
- gi No. 100934

- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9770
- gi No. 100934
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9771
- gi No. 100934
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9772
- gi No. 100934
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9773
- gi No. 100981
- % Identity 100
- Alignment Length 34
- Location of Alignment in SEQ ID NO 1320: from 113 to 146
  
- Alignment No. 9774
- gi No. 100981
- % Identity 100
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1320: from 37 to 76
  
- Alignment No. 9775
- gi No. 102062
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9776
- gi No. 102062
- % Identity 92.2
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
  
- Alignment No. 9777
- gi No. 102278
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9778
- gi No. 102278
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9779
- gi No. 102278
- % Identity 94.5

- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9780
- gi No. 102278
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9781
- gi No. 102278
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9782
- gi No. 102278
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9783
- gi No. 102278
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9784
- gi No. 102279
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9785
- gi No. 102279
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9786
- gi No. 102279
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9787
- gi No. 102280
- % Identity 93.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9788
- gi No. 102280
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9789
- gi No. 102280
- % Identity 93.2
- Alignment Length 146

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- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9790
- gi No. 102280
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9791
- gi No. 102280
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9792
- gi No. 102281
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 9793
- gi No. 102281
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9794
- gi No. 102281
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9795
- gi No. 102281
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9796
- gi No. 102281
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9797
- gi No. 102389
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 9798
- gi No. 102389
- % Identity 85.2
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1320: from 1 to 87
- Alignment No. 9799
- gi No. 103436
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

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- Alignment No. 9800
- gi No. 103436
- % Identity 94.8
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
  
- Alignment No. 9801
- gi No. 1044940
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9802
- gi No. 1044940
- % Identity 98.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9803
- gi No. 104829
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9804
- gi No. 104829
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9805
- gi No. 104829
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9806
- gi No. 1050930
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9807
- gi No. 1050930
- % Identity 95
- Alignment Length 100
- Location of Alignment in SEQ ID NO 1320: from 1 to 100
  
- Alignment No. 9808
- gi No. 10673
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9809
- gi No. 10673
- % Identity 87.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1320: from 1 to 87

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- Alignment No. 9810
- gi No. 1070590
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9811
- gi No. 1070590
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9812
- gi No. 1070590
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9813
- gi No. 1070591
- % Identity 94.8
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
  
- Alignment No. 9814
- gi No. 1070591
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9815
- gi No. 1070591
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9816
- gi No. 1070591
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9817
- gi No. 1070591
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9818
- gi No. 1070591
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9819
- gi No. 1070591
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9820

- gi No. 1070591
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9821
- gi No. 1070591
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9822
- gi No. 1076678
- % Identity 98.7
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 9823
- gi No. 1076678
- % Identity 79.2
- Alignment Length 96
- Location of Alignment in SEQ ID NO 1320: from 54 to 146
- Alignment No. 9824
- gi No. 1076708
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 9825
- gi No. 1076708
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9826
- gi No. 1076708
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9827
- gi No. 1076708
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9828
- gi No. 1078777
- % Identity 87.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 9829
- gi No. 1078777
- % Identity 88.2
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 9830
- gi No. 1078813

- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9831
- gi No. 1078813
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9832
- gi No. 1078813
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9833
- gi No. 1083758
- % Identity 88
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1320: from 1 to 108
  
- Alignment No. 9834
- gi No. 1083758
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9835
- gi No. 1083758
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9836
- gi No. 1083758
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9837
- gi No. 1083758
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9838
- gi No. 1083758
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9839
- gi No. 1083758
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9840
- gi No. 1083758
- % Identity 95.9

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- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9841
- gi No. 1083758
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9842
- gi No. 1083758
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9843
- gi No. 1101011
- % Identity 84.2
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9844
- gi No. 1101011
- % Identity 87.3
- Alignment Length 79
- Location of Alignment in SEQ ID NO 1320: from 68 to 146
  
- Alignment No. 9845
- gi No. 1101011
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9846
- gi No. 1101011
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9847
- gi No. 1101011
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9848
- gi No. 1101011
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9849
- gi No. 1101011
- % Identity 84.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9850
- gi No. 1101011
- % Identity 86.3
- Alignment Length 146

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- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9851
- gi No. 1101011
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9852
- gi No. 1101011
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9853
- gi No. 1101011
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9854
- gi No. 1101013
- % Identity 85
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1320: from 7 to 46
- Alignment No. 9855
- gi No. 1101013
- % Identity 85
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1320: from 83 to 122
- Alignment No. 9856
- gi No. 1101015
- % Identity 85
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1320: from 7 to 46
- Alignment No. 9857
- gi No. 1101015
- % Identity 85
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1320: from 83 to 122
- Alignment No. 9858
- gi No. 1101019
- % Identity 80
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1320: from 7 to 46
- Alignment No. 9859
- gi No. 1101019
- % Identity 80
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1320: from 83 to 122
- Alignment No. 9860
- gi No. 1101021
- % Identity 87
- Alignment Length 46
- Location of Alignment in SEQ ID NO 1320: from 1 to 46

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- Alignment No. 9861
- gi No. 1101021
- % Identity 84.4
- Alignment Length 64
- Location of Alignment in SEQ ID NO 1320: from 83 to 146
  
- Alignment No. 9862
- gi No. 1101021
- % Identity 86.2
- Alignment Length 116
- Location of Alignment in SEQ ID NO 1320: from 7 to 122
  
- Alignment No. 9863
- gi No. 1101023
- % Identity 87.9
- Alignment Length 33
- Location of Alignment in SEQ ID NO 1320: from 114 to 146
  
- Alignment No. 9864
- gi No. 1101023
- % Identity 92
- Alignment Length 50
- Location of Alignment in SEQ ID NO 1320: from 38 to 87
  
- Alignment No. 9865
- gi No. 1107481
- % Identity 97.9
- Alignment Length 96
- Location of Alignment in SEQ ID NO 1320: from 1 to 96
  
- Alignment No. 9866
- gi No. 1107481
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9867
- gi No. 1143188
- % Identity 94.5
- Alignment Length 73
- Location of Alignment in SEQ ID NO 1320: from 77 to 149
  
- Alignment No. 9868
- gi No. 1143188
- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9869
- gi No. 1143188
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9870
- gi No. 1143188
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9871
- gi No. 1167510
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 9872
- gi No. 1167510
- % Identity 91.3
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1320: from 1 to 103
- Alignment No. 9873
- gi No. 1174858
- % Identity 74.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 9874
- gi No. 1174858
- % Identity 76.3
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 9875
- gi No. 1174859
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 9876
- gi No. 1174859
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 9877
- gi No. 1174860
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 9878
- gi No. 1174860
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 9879
- gi No. 1174861
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 9880
- gi No. 1174861
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 9881



- gi No. 1184755
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9882
- gi No. 1184755
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9883
- gi No. 1197093
- % Identity 94.8
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
  
- Alignment No. 9884
- gi No. 1197093
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9885
- gi No. 1197093
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9886
- gi No. 1197093
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9887
- gi No. 1304128
- % Identity 96.2
- Alignment Length 79
- Location of Alignment in SEQ ID NO 1320: from 1 to 79
  
- Alignment No. 9888
- gi No. 1304128
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9889
- gi No. 1304128
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9890
- gi No. 1304128
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9891
- gi No. 1304128

- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9892
- gi No. 1304128
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9893
- gi No. 1304128
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9894
- gi No. 1304128
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9895
- gi No. 1304357
- % Identity 81.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9896
- gi No. 1304357
- % Identity 82.9
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9897
- gi No. 1321735
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9898
- gi No. 1321735
- % Identity 95.7
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1320: from 1 to 139
  
- Alignment No. 9899
- gi No. 1326021
- % Identity 96.3
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1320: from 120 to 146
  
- Alignment No. 9900
- gi No. 1326021
- % Identity 97
- Alignment Length 33
- Location of Alignment in SEQ ID NO 1320: from 44 to 76
  
- Alignment No. 9901
- gi No. 1326022
- % Identity 96.1

- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9902
- gi No. 1326022
- % Identity 97.2
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1320: from 39 to 146
  
- Alignment No. 9903
- gi No. 1326022
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9904
- gi No. 1332579
- % Identity 97.4
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
  
- Alignment No. 9905
- gi No. 1332579
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9906
- gi No. 1332579
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9907
- gi No. 1332579
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9908
- gi No. 1332579
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9909
- gi No. 1332579
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9910
- gi No. 1332579
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9911
- gi No. 1332579
- % Identity 100
- Alignment Length 146

- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9912
- gi No. 1332579
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9913
- gi No. 1332579
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9914
- gi No. 1351348
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 9915
- gi No. 1351348
- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 9916
- gi No. 1351349
- % Identity 90
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 9917
- gi No. 1351349
- % Identity 90.8
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 9918
- gi No. 1353755
- % Identity 95.2
- Alignment Length 83
- Location of Alignment in SEQ ID NO 1320: from 1 to 83
- Alignment No. 9919
- gi No. 1353755
- % Identity 95.2
- Alignment Length 105
- Location of Alignment in SEQ ID NO 1320: from 42 to 146
- Alignment No. 9920
- gi No. 1353757
- % Identity 93.5
- Alignment Length 46
- Location of Alignment in SEQ ID NO 1320: from 1 to 46
- Alignment No. 9921
- gi No. 1353757
- % Identity 94.2
- Alignment Length 69
- Location of Alignment in SEQ ID NO 1320: from 78 to 146

- Alignment No. 9922
- gi No. 1353757
- % Identity 94.2
- Alignment Length 121
- Location of Alignment in SEQ ID NO 1320: from 2 to 122
  
- Alignment No. 9923
- gi No. 1362008
- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9924
- gi No. 1362008
- % Identity 92.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9925
- gi No. 1362008
- % Identity 92.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9926
- gi No. 1362008
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9927
- gi No. 1362008
- % Identity 92.5
- Alignment Length 159
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9928
- gi No. 1362009
- % Identity 79.7
- Alignment Length 148
- Location of Alignment in SEQ ID NO 1320: from 1 to 148
  
- Alignment No. 9929
- gi No. 1362010
- % Identity 92.2
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9930
- gi No. 1362010
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9931
- gi No. 1362010
- % Identity 88.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

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- Alignment No. 9932
- gi No. 1362010
- % Identity 92.5
- Alignment Length 147
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9933
- gi No. 1362012
- % Identity 89.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9934
- gi No. 1362012
- % Identity 76.2
- Alignment Length 149
- Location of Alignment in SEQ ID NO 1320: from 1 to 147
  
- Alignment No. 9935
- gi No. 1362012
- % Identity 79.6
- Alignment Length 152
- Location of Alignment in SEQ ID NO 1320: from 1 to 145
  
- Alignment No. 9936
- gi No. 1362012
- % Identity 71.1
- Alignment Length 167
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9937
- gi No. 136665
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9938
- gi No. 136665
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9939
- gi No. 136666
- % Identity 98.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9940
- gi No. 136666
- % Identity 98.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9941
- gi No. 136667
- % Identity 98.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9942

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- gi No. 136667
- % Identity 98.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9943
- gi No. 136668
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9944
- gi No. 136668
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9945
- gi No. 136669
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9946
- gi No. 136669
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9947
- gi No. 136670
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9948
- gi No. 136670
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9949
- gi No. 136671
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9950
- gi No. 136671
- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9951
- gi No. 136672
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9952
- gi No. 136672

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- % Identity 93.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9953
- gi No. 136673
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9954
- gi No. 136673
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9955
- gi No. 136674
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9956
- gi No. 136674
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9957
- gi No. 136675
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9958
- gi No. 136675
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9959
- gi No. 136676
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9960
- gi No. 136676
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9961
- gi No. 136677
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9962
- gi No. 136677
- % Identity 97.4



- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9963
- gi No. 136678
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9964
- gi No. 136678
- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9965
- gi No. 1421797
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9966
- gi No. 1421797
- % Identity 96.2
- Alignment Length 79
- Location of Alignment in SEQ ID NO 1320: from 1 to 79
  
- Alignment No. 9967
- gi No. 1480012
- % Identity 96.3
- Alignment Length 54
- Location of Alignment in SEQ ID NO 1320: from 93 to 146
  
- Alignment No. 9968
- gi No. 1480012
- % Identity 95.1
- Alignment Length 61
- Location of Alignment in SEQ ID NO 1320: from 17 to 77
  
- Alignment No. 9969
- gi No. 156480
- % Identity 94.6
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1320: from 1 to 37
  
- Alignment No. 9970
- gi No. 156480
- % Identity 94.6
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1320: from 77 to 113
  
- Alignment No. 9971
- gi No. 158759
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9972
- gi No. 158759
- % Identity 94.7
- Alignment Length 76

- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 9973
- gi No. 158763
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 9974
- gi No. 158763
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 9975
- gi No. 158765
- % Identity 91.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 9976
- gi No. 158765
- % Identity 92.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 9977
- gi No. 158767
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 9978
- gi No. 158767
- % Identity 93.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 9979
- gi No. 158769
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 9980
- gi No. 158769
- % Identity 93.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 9981
- gi No. 158771
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 9982
- gi No. 158771
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

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- Alignment No. 9983
- gi No. 161281
- % Identity 94.4
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1320: from 77 to 147
- Alignment No. 9984
- gi No. 161281
- % Identity 93.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 9985
- gi No. 163575
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 9986
- gi No. 163575
- % Identity 96.3
- Alignment Length 81
- Location of Alignment in SEQ ID NO 1320: from 66 to 146
- Alignment No. 9987
- gi No. 163575
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9988
- gi No. 166336
- % Identity 96.1
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
- Alignment No. 9989
- gi No. 166336
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9990
- gi No. 166336
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9991
- gi No. 166336
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9992
- gi No. 166336
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9993
- gi No. 166336
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 9994
- gi No. 1666175
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 9995
- gi No. 1666175
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9996
- gi No. 1675359
- % Identity 92.7
- Alignment Length 41
- Location of Alignment in SEQ ID NO 1320: from 1 to 41
  
- Alignment No. 9997
- gi No. 1675359
- % Identity 92.7
- Alignment Length 41
- Location of Alignment in SEQ ID NO 1320: from 77 to 117
  
- Alignment No. 9998
- gi No. 167935
- % Identity 93.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 9999
- gi No. 167935
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10000
- gi No. 167935
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10001
- gi No. 167935
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10002
- gi No. 167935
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10003

- gi No. 167941
- % Identity 92.8
- Alignment Length 69
- Location of Alignment in SEQ ID NO 1320: from 78 to 146
  
- Alignment No. 10004
- gi No. 167941
- % Identity 93.3
- Alignment Length 75
- Location of Alignment in SEQ ID NO 1320: from 2 to 76
  
- Alignment No. 10005
- gi No. 167945
- % Identity 93.5
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
  
- Alignment No. 10006
- gi No. 167945
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10007
- gi No. 167945
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10008
- gi No. 167947
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10009
- gi No. 167947
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10010
- gi No. 167947
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10011
- gi No. 167947
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10012
- gi No. 167947
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10013
- gi No. 167947

- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10014
- gi No. 167947
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10015
- gi No. 167949
- % Identity 93.5
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
  
- Alignment No. 10016
- gi No. 167949
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10017
- gi No. 167949
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10018
- gi No. 167949
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10019
- gi No. 167949
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10020
- gi No. 1684855
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10021
- gi No. 1684855
- % Identity 81.7
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1320: from 16 to 146
  
- Alignment No. 10022
- gi No. 1684855
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10023
- gi No. 1684855
- % Identity 100

- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10024
- gi No. 1684855
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10025
- gi No. 1684857
- % Identity 98.7
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
  
- Alignment No. 10026
- gi No. 1684857
- % Identity 100
- Alignment Length 132
- Location of Alignment in SEQ ID NO 1320: from 15 to 146
  
- Alignment No. 10027
- gi No. 1684857
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10028
- gi No. 170352
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10029
- gi No. 170352
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10030
- gi No. 170352
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10031
- gi No. 170352
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10032
- gi No. 170352
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10033
- gi No. 170352
- % Identity 100
- Alignment Length 146

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- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10034
- gi No. 170354
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10035
- gi No. 170354
- % Identity 100
- Alignment Length 142
- Location of Alignment in SEQ ID NO 1320: from 5 to 146
- Alignment No. 10036
- gi No. 170354
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10037
- gi No. 170354
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10038
- gi No. 170354
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10039
- gi No. 1762374
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10040
- gi No. 1762374
- % Identity 95.8
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1320: from 1 to 71
- Alignment No. 10041
- gi No. 1762935
- % Identity 98.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10042
- gi No. 1762935
- % Identity 98.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10043
- gi No. 1763015
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146



- Alignment No. 10044
- gi No. 1763015
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10045
- gi No. 1771780
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10046
- gi No. 1771780
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10047
- gi No. 1778712
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10048
- gi No. 1778712
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10049
- gi No. 1778712
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10050
- gi No. 1778712
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10051
- gi No. 1778712
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10052
- gi No. 1800281
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10053
- gi No. 1800281
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

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- Alignment No. 10054
- gi No. 1800281
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10055
- gi No. 1800281
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10056
- gi No. 1800281
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10057
- gi No. 1805696
- % Identity 95.2
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1320: from 84 to 146
- Alignment No. 10058
- gi No. 1805696
- % Identity 95.4
- Alignment Length 65
- Location of Alignment in SEQ ID NO 1320: from 1 to 65
- Alignment No. 10059
- gi No. 1805696
- % Identity 95.5
- Alignment Length 134
- Location of Alignment in SEQ ID NO 1320: from 8 to 141
- Alignment No. 10060
- gi No. 1839584
- % Identity 100
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1320: from 1 to 38
- Alignment No. 10061
- gi No. 1839584
- % Identity 100
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1320: from 77 to 114
- Alignment No. 10062
- gi No. 1841849
- % Identity 100
- Alignment Length 16
- Location of Alignment in SEQ ID NO 1320: from 1 to 16
- Alignment No. 10063
- gi No. 1841849
- % Identity 100
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1320: from 112 to 146
- Alignment No. 10064

- gi No. 1841849
- % Identity 100
- Alignment Length 57
- Location of Alignment in SEQ ID NO 1320: from 36 to 92
  
- Alignment No. 10065
- gi No. 208558
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10066
- gi No. 208558
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10067
- gi No. 208560
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10068
- gi No. 208560
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10069
- gi No. 208562
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10070
- gi No. 208562
- % Identity 93.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10071
- gi No. 208564
- % Identity 91.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10072
- gi No. 208564
- % Identity 92.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10073
- gi No. 208566
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10074
- gi No. 208566

- % Identity 93.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10075
- gi No. 208568
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10076
- gi No. 208568
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10077
- gi No. 208891
- % Identity 96
- Alignment Length 75
- Location of Alignment in SEQ ID NO 1320: from 72 to 146
- Alignment No. 10078
- gi No. 208891
- % Identity 93.9
- Alignment Length 98
- Location of Alignment in SEQ ID NO 1320: from 1 to 98
- Alignment No. 10079
- gi No. 209603
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10080
- gi No. 209603
- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10081
- gi No. 2118958
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10082
- gi No. 2118958
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10083
- gi No. 2118958
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10084
- gi No. 2118958
- % Identity 95.9

- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10085
- gi No. 2118958
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10086
- gi No. 2118959
- % Identity 85.7
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1320: from 1 to 112
  
- Alignment No. 10087
- gi No. 2118959
- % Identity 84.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10088
- gi No. 2118959
- % Identity 83.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10089
- gi No. 2118960
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10090
- gi No. 2118960
- % Identity 96.5
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1320: from 62 to 146
  
- Alignment No. 10091
- gi No. 2118960
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10092
- gi No. 2118961
- % Identity 94.6
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1320: from 73 to 146
  
- Alignment No. 10093
- gi No. 2118961
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10094
- gi No. 2118961
- % Identity 95.2
- Alignment Length 146

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- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10095
- gi No. 2118962
- % Identity 95.9
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1320: from 73 to 146
- Alignment No. 10096
- gi No. 2118962
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10097
- gi No. 2118962
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10098
- gi No. 2118963
- % Identity 89.3
- Alignment Length 75
- Location of Alignment in SEQ ID NO 1320: from 1 to 75
- Alignment No. 10099
- gi No. 2118963
- % Identity 91
- Alignment Length 111
- Location of Alignment in SEQ ID NO 1320: from 36 to 146
- Alignment No. 10100
- gi No. 2118964
- % Identity 94.8
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
- Alignment No. 10101
- gi No. 2118964
- % Identity 96.4
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1320: from 37 to 146
- Alignment No. 10102
- gi No. 2118964
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10103
- gi No. 2118964
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10104
- gi No. 2118965
- % Identity 94.8
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77

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- Alignment No. 10105
- gi No. 2118965
- % Identity 96.3
- Alignment Length 81
- Location of Alignment in SEQ ID NO 1320: from 66 to 146
- Alignment No. 10106
- gi No. 2118965
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10107
- gi No. 2118965
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10108
- gi No. 2129452
- % Identity 93.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10109
- gi No. 2129452
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10110
- gi No. 2129452
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10111
- gi No. 2129452
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10112
- gi No. 2129452
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10113
- gi No. 2129452
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10114
- gi No. 2133278
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10115
- gi No. 2133278
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10116
- gi No. 2133549
- % Identity 96.3
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1320: from 120 to 146
  
- Alignment No. 10117
- gi No. 2133549
- % Identity 95.8
- Alignment Length 48
- Location of Alignment in SEQ ID NO 1320: from 1 to 48
  
- Alignment No. 10118
- gi No. 2133549
- % Identity 96
- Alignment Length 50
- Location of Alignment in SEQ ID NO 1320: from 97 to 146
  
- Alignment No. 10119
- gi No. 2133549
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1320: from 21 to 76
  
- Alignment No. 10120
- gi No. 2133549
- % Identity 96.3
- Alignment Length 81
- Location of Alignment in SEQ ID NO 1320: from 44 to 124
  
- Alignment No. 10121
- gi No. 2144011
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10122
- gi No. 2144011
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10123
- gi No. 2144275
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10124
- gi No. 2144275
- % Identity 92.2
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
  
- Alignment No. 10125



- gi No. 2144734
- % Identity 87.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1320: from 1 to 87
  
- Alignment No. 10126
- gi No. 2144734
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10127
- gi No. 2144734
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10128
- gi No. 2144734
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10129
- gi No. 2149467
- % Identity 87.7
- Alignment Length 83
- Location of Alignment in SEQ ID NO 1320: from 68 to 146
  
- Alignment No. 10130
- gi No. 2149467
- % Identity 83.3
- Alignment Length 90
- Location of Alignment in SEQ ID NO 1320: from 1 to 85
  
- Alignment No. 10131
- gi No. 2209091
- % Identity 93.5
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
  
- Alignment No. 10132
- gi No. 2209091
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10133
- gi No. 223061
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10134
- gi No. 223061
- % Identity 94.7
- Alignment Length 75
- Location of Alignment in SEQ ID NO 1320: from 1 to 75
  
- Alignment No. 10135
- gi No. 224321

- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10136
- gi No. 224321
- % Identity 97.2
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1320: from 39 to 146
  
- Alignment No. 10137
- gi No. 224321
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10138
- gi No. 225317
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 1 to 70
  
- Alignment No. 10139
- gi No. 225317
- % Identity 89.6
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 77 to 153
  
- Alignment No. 10140
- gi No. 225319
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 1 to 70
  
- Alignment No. 10141
- gi No. 225319
- % Identity 89.6
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 77 to 153
  
- Alignment No. 10142
- gi No. 225320
- % Identity 91.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 1 to 70
  
- Alignment No. 10143
- gi No. 225320
- % Identity 87
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 77 to 153
  
- Alignment No. 10144
- gi No. 2281952
- % Identity 95.2
- Alignment Length 62
- Location of Alignment in SEQ ID NO 1320: from 8 to 69
  
- Alignment No. 10145
- gi No. 2281952
- % Identity 95.2

- Alignment Length 62
- Location of Alignment in SEQ ID NO 1320: from 84 to 145
  
- Alignment No. 10146
- gi No. 2281954
- % Identity 93.5
- Alignment Length 62
- Location of Alignment in SEQ ID NO 1320: from 8 to 69
  
- Alignment No. 10147
- gi No. 2281954
- % Identity 93.5
- Alignment Length 62
- Location of Alignment in SEQ ID NO 1320: from 84 to 145
  
- Alignment No. 10148
- gi No. 2281955
- % Identity 88.9
- Alignment Length 45
- Location of Alignment in SEQ ID NO 1320: from 8 to 52
  
- Alignment No. 10149
- gi No. 2281955
- % Identity 88.9
- Alignment Length 45
- Location of Alignment in SEQ ID NO 1320: from 84 to 128
  
- Alignment No. 10150
- gi No. 2281959
- % Identity 90.6
- Alignment Length 64
- Location of Alignment in SEQ ID NO 1320: from 83 to 146
  
- Alignment No. 10151
- gi No. 2281959
- % Identity 90.8
- Alignment Length 65
- Location of Alignment in SEQ ID NO 1320: from 7 to 71
  
- Alignment No. 10152
- gi No. 2330875
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10153
- gi No. 2330875
- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10154
- gi No. 2350864
- % Identity 75.9
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1320: from 6 to 63
  
- Alignment No. 10155
- gi No. 2350864
- % Identity 75.9
- Alignment Length 58

- Location of Alignment in SEQ ID NO 1320: from 82 to 139
- Alignment No. 10156
- gi No. 2408009
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10157
- gi No. 2408009
- % Identity 87.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1320: from 1 to 87
- Alignment No. 10158
- gi No. 2437825
- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10159
- gi No. 2437825
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10160
- gi No. 2437825
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10161
- gi No. 2437825
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10162
- gi No. 247308
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10163
- gi No. 247308
- % Identity 90.8
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10164
- gi No. 248865
- % Identity 95
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1320: from 1 to 20
- Alignment No. 10165
- gi No. 248865
- % Identity 95
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1320: from 77 to 96

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- Alignment No. 10166
- gi No. 2558539
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10167
- gi No. 2558539
- % Identity 94.8
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
  
- Alignment No. 10168
- gi No. 2627129
- % Identity 94.8
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
  
- Alignment No. 10169
- gi No. 2627129
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10170
- gi No. 2627129
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10171
- gi No. 2627129
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10172
- gi No. 2627129
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10173
- gi No. 2627129
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10174
- gi No. 2627129
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10175
- gi No. 2627129
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10176
- gi No. 2627131
- % Identity 89.8
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1320: from 1 to 108
  
- Alignment No. 10177
- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10178
- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10179
- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10180
- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10181
- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10182
- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10183
- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10184
- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10185
- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10186

- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10187
- gi No. 2627133
- % Identity 89.8
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1320: from 1 to 108
  
- Alignment No. 10188
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10189
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10190
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10191
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10192
- gi No. 2627133
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10193
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10194
- gi No. 2627133
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10195
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10196
- gi No. 2627133

- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10197
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10198
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10199
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10200
- gi No. 2641213
- % Identity 98.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
  
- Alignment No. 10201
- gi No. 2641213
- % Identity 98.6
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1320: from 1 to 139
  
- Alignment No. 10202
- gi No. 2654141
- % Identity 92.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10203
- gi No. 2654141
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10204
- gi No. 2654141
- % Identity 91.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10205
- gi No. 2654141
- % Identity 89
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10206
- gi No. 2654141
- % Identity 89.7

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- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10207
- gi No. 2707837
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10208
- gi No. 2707837
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10209
- gi No. 2707837
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10210
- gi No. 2707837
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10211
- gi No. 2739333
- % Identity 97.4
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
  
- Alignment No. 10212
- gi No. 2739333
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10213
- gi No. 2739333
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10214
- gi No. 2739333
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
  
- Alignment No. 10215
- gi No. 2760345
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
  
- Alignment No. 10216
- gi No. 2760345
- % Identity 100
- Alignment Length 146

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- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10217
- gi No. 2760345
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10218
- gi No. 2760345
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10219
- gi No. 2760347
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10220
- gi No. 2760347
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10221
- gi No. 2760347
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10222
- gi No. 2760347
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10223
- gi No. 2760347
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10224
- gi No. 2760347
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10225
- gi No. 2760349
- % Identity 98.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10226
- gi No. 2760349
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

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- Alignment No. 10227
- gi No. 2760349
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10228
- gi No. 2760349
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10229
- gi No. 2760349
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10230
- gi No. 279635
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10231
- gi No. 279635
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10232
- gi No. 279636
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10233
- gi No. 279636
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10234
- gi No. 280386
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10235
- gi No. 280386
- % Identity 98.7
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77

- Alignment No. 10236
- gi No. 281276
- % Identity 90
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1320: from 1 to 20

- Alignment No. 10237
- gi No. 281276
- % Identity 90
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1320: from 77 to 96

- Alignment No. 10238
- gi No. 283496
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10239
- gi No. 283496
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10240
- gi No. 283496
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10241
- gi No. 283496
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10242
- gi No. 283496
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10243
- gi No. 2894304
- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10244
- gi No. 2894304
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10245
- gi No. 2894304
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10246
- gi No. 2894304
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10247

- gi No. 2894306
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10248
- gi No. 2894306
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10249
- gi No. 2894308
- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10250
- gi No. 2894308
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10251
- gi No. 2894308
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10252
- gi No. 2894308
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10253
- gi No. 2894308
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10254
- gi No. 2995277
- % Identity 100
- Alignment Length 23
- Location of Alignment in SEQ ID NO 1320: from 124 to 146

- Alignment No. 10255
- gi No. 2995277
- % Identity 96.7
- Alignment Length 30
- Location of Alignment in SEQ ID NO 1320: from 48 to 77

- Alignment No. 10256
- gi No. 2995949
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10257
- gi No. 2995949

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- % Identity 100
- Alignment Length 104
- Location of Alignment in SEQ ID NO 1320: from 43 to 146
- Alignment No. 10258
- gi No. 3047314
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10259
- gi No. 3047314
- % Identity 87.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1320: from 1 to 87
- Alignment No. 10260
- gi No. 3047316
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10261
- gi No. 3047316
- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10262
- gi No. 3047318
- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10263
- gi No. 3047318
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10264
- gi No. 3047318
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10265
- gi No. 3047318
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10266
- gi No. 3047318
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10267
- gi No. 3091264
- % Identity 98.7

- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10268
- gi No. 3091264
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10269
- gi No. 3091264
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10270
- gi No. 3091264
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10271
- gi No. 3126967
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10272
- gi No. 3126967
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10273
- gi No. 3126967
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10274
- gi No. 3126967
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10275
- gi No. 3126967
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10276
- gi No. 3126967
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10277
- gi No. 3152950
- % Identity 97.1
- Alignment Length 70

- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10278
- gi No. 3152950
- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10279
- gi No. 3158372
- % Identity 100
- Alignment Length 98
- Location of Alignment in SEQ ID NO 1320: from 49 to 146
- Alignment No. 10280
- gi No. 3158372
- % Identity 99.1
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1320: from 1 to 109
- Alignment No. 10281
- gi No. 320608
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10282
- gi No. 320608
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10283
- gi No. 320608
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10284
- gi No. 320608
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10285
- gi No. 322750
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10286
- gi No. 322750
- % Identity 98.7
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
- Alignment No. 10287
- gi No. 323071
- % Identity 84.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10288
- gi No. 323071
- % Identity 85.5
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10289
- gi No. 323157
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10290
- gi No. 323157
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10291
- gi No. 323157
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10292
- gi No. 323157
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10293
- gi No. 323157
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10294
- gi No. 323157
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10295
- gi No. 323208
- % Identity 88.2
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1320: from 1 to 85

- Alignment No. 10296
- gi No. 323208
- % Identity 82.5
- Alignment Length 144
- Location of Alignment in SEQ ID NO 1320: from 4 to 146

- Alignment No. 10297
- gi No. 323230
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10298
- gi No. 323230
- % Identity 83.7
- Alignment Length 86
- Location of Alignment in SEQ ID NO 1320: from 1 to 85

- Alignment No. 10299
- gi No. 3265058
- % Identity 98.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10300
- gi No. 3265058
- % Identity 98.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10301
- gi No. 3319208
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10302
- gi No. 3319208
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10303
- gi No. 3335355
- % Identity 100
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1320: from 132 to 146

- Alignment No. 10304
- gi No. 3335355
- % Identity 100
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1320: from 56 to 76

- Alignment No. 10305
- gi No. 3335355
- % Identity 97.7
- Alignment Length 129
- Location of Alignment in SEQ ID NO 1320: from 1 to 129

- Alignment No. 10306
- gi No. 3335355
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10307
- gi No. 3335355
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10308

- gi No. 340062
- % Identity 95.5
- Alignment Length 66
- Location of Alignment in SEQ ID NO 1320: from 81 to 146

- Alignment No. 10309
- gi No. 340062
- % Identity 95.8
- Alignment Length 72
- Location of Alignment in SEQ ID NO 1320: from 5 to 76

- Alignment No. 10310
- gi No. 3452083
- % Identity 93.1
- Alignment Length 29
- Location of Alignment in SEQ ID NO 1320: from 1 to 29

- Alignment No. 10311
- gi No. 3452083
- % Identity 97.9
- Alignment Length 48
- Location of Alignment in SEQ ID NO 1320: from 99 to 146

- Alignment No. 10312
- gi No. 3452083
- % Identity 96.4
- Alignment Length 83
- Location of Alignment in SEQ ID NO 1320: from 23 to 105

- Alignment No. 10313
- gi No. 348148
- % Identity 96.3
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1320: from 120 to 146

- Alignment No. 10314
- gi No. 348148
- % Identity 95.8
- Alignment Length 48
- Location of Alignment in SEQ ID NO 1320: from 1 to 48

- Alignment No. 10315
- gi No. 348148
- % Identity 96.3
- Alignment Length 81
- Location of Alignment in SEQ ID NO 1320: from 44 to 124

- Alignment No. 10316
- gi No. 348149
- % Identity 96
- Alignment Length 50
- Location of Alignment in SEQ ID NO 1320: from 97 to 146

- Alignment No. 10317
- gi No. 348149
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1320: from 21 to 76

- Alignment No. 10318
- gi No. 3603456

- % Identity 98.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10319
- gi No. 3603456
- % Identity 100
- Alignment Length 106
- Location of Alignment in SEQ ID NO 1320: from 41 to 146
- Alignment No. 10320
- gi No. 3603456
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10321
- gi No. 3603456
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10322
- gi No. 3687425
- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10323
- gi No. 3687425
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10324
- gi No. 3687425
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10325
- gi No. 3738185
- % Identity 96.1
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
- Alignment No. 10326
- gi No. 3738185
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10327
- gi No. 3738185
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10328
- gi No. 3738185
- % Identity 97.3

- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10329
- gi No. 3738185
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10330
- gi No. 3776536
- % Identity 96.1
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77

- Alignment No. 10331
- gi No. 3776536
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10332
- gi No. 3776536
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10333
- gi No. 3776536
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10334
- gi No. 3776536
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10335
- gi No. 3776536
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10336
- gi No. 3776536
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10337
- gi No. 3776536
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10338
- gi No. 3789940
- % Identity 100
- Alignment Length 76

- [illegible]

- Alignment No. 10349
- gi No. 385076
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10350
- gi No. 385076
- % Identity 93.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10351
- gi No. 3882081
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10352
- gi No. 3882081
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10353
- gi No. 3882081
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10354
- gi No. 3885463
- % Identity 94
- Alignment Length 67
- Location of Alignment in SEQ ID NO 1320: from 80 to 146

- Alignment No. 10355
- gi No. 3885463
- % Identity 86.6
- Alignment Length 82
- Location of Alignment in SEQ ID NO 1320: from 4 to 85

- Alignment No. 10356
- gi No. 3892189
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10357
- gi No. 3892189
- % Identity 84.1
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1320: from 1 to 87

- Alignment No. 10358
- gi No. 402242
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10359
- gi No. 402242
- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10360
- gi No. 4049712
- % Identity 85.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10361
- gi No. 4049712
- % Identity 84.6
- Alignment Length 78
- Location of Alignment in SEQ ID NO 1320: from 1 to 78

- Alignment No. 10362
- gi No. 4102845
- % Identity 86.2
- Alignment Length 65
- Location of Alignment in SEQ ID NO 1320: from 82 to 146

- Alignment No. 10363
- gi No. 4102845
- % Identity 87.3
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1320: from 6 to 76

- Alignment No. 10364
- gi No. 4105408
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10365
- gi No. 4105408
- % Identity 95.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 1320: from 10 to 146

- Alignment No. 10366
- gi No. 4105408
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10367
- gi No. 4105408
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10368
- gi No. 4115337
- % Identity 98.7
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77

- Alignment No. 10369

- gi No. 4115337
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10370
- gi No. 4115337
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10371
- gi No. 4115337
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10372
- gi No. 4115337
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10373
- gi No. 4115337
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10374
- gi No. 4150898
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10375
- gi No. 4150898
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10376
- gi No. 4150898
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10377
- gi No. 4150898
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10378
- gi No. 4150912
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10379
- gi No. 4150912

- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10380
- gi No. 4150912
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10381
- gi No. 4150912
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10382
- gi No. 4150912
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10383
- gi No. 4150914
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10384
- gi No. 4150914
- % Identity 95.7
- Alignment Length 140
- Location of Alignment in SEQ ID NO 1320: from 7 to 146

- Alignment No. 10385
- gi No. 4151082
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10386
- gi No. 4151082
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10387
- gi No. 418854
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10388
- gi No. 418854
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10389
- gi No. 418854
- % Identity 100

- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10390
- gi No. 418854
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10391
- gi No. 418854
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10392
- gi No. 418854
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10393
- gi No. 421735
- % Identity 94.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 1320: from 1 to 19
- Alignment No. 10394
- gi No. 421735
- % Identity 94.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 1320: from 77 to 95
- Alignment No. 10395
- gi No. 421867
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10396
- gi No. 421867
- % Identity 98.7
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
- Alignment No. 10397
- gi No. 421929
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10398
- gi No. 421929
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10399
- gi No. 421929
- % Identity 99.3
- Alignment Length 146

- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10400
- gi No. 421929
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10401
- gi No. 421929
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10402
- gi No. 421929
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10403
- gi No. 421929
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10404
- gi No. 422248
- % Identity 97.4
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
- Alignment No. 10405
- gi No. 422248
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10406
- gi No. 422248
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10407
- gi No. 422248
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10408
- gi No. 422248
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10409
- gi No. 422269
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10410
- gi No. 422269
- % Identity 93.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10411
- gi No. 422270
- % Identity 90
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10412
- gi No. 422270
- % Identity 89.6
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77

- Alignment No. 10413
- gi No. 422271
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10414
- gi No. 422271
- % Identity 92.2
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77

- Alignment No. 10415
- gi No. 433970
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10416
- gi No. 433970
- % Identity 95.5
- Alignment Length 111
- Location of Alignment in SEQ ID NO 1320: from 36 to 146

- Alignment No. 10417
- gi No. 433970
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10418
- gi No. 433970
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10419
- gi No. 433970
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10420
- gi No. 433970
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10421
- gi No. 444791
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10422
- gi No. 444791
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10423
- gi No. 444791
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10424
- gi No. 444791
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10425
- gi No. 4506713
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10426
- gi No. 4506713
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10427
- gi No. 4507761
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10428
- gi No. 4507761
- % Identity 94.8
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77

- Alignment No. 10429
- gi No. 4510359
- % Identity 100
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1320: from 112 to 146

- Alignment No. 10430

- gi No. 4510359
- % Identity 97.6
- Alignment Length 42
- Location of Alignment in SEQ ID NO 1320: from 36 to 77

- Alignment No. 10431
- gi No. 456779
- % Identity 92
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1320: from 1 to 25

- Alignment No. 10432
- gi No. 456779
- % Identity 92
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1320: from 77 to 101

- Alignment No. 10433
- gi No. 4586594
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10434
- gi No. 4586594
- % Identity 100
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1320: from 1 to 108

- Alignment No. 10435
- gi No. 4587232
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10436
- gi No. 4587232
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10437
- gi No. 4587234
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10438
- gi No. 4587234
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10439
- gi No. 4587236
- % Identity 96.1
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77

- Alignment No. 10440
- gi No. 4587236

- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10441
- gi No. 4587236
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10442
- gi No. 4587236
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10443
- gi No. 4587236
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10444
- gi No. 4587236
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10445
- gi No. 4587236
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10446
- gi No. 4587236
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10447
- gi No. 4587236
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10448
- gi No. 4587236
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10449
- gi No. 4587236
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10450
- gi No. 4587236
- % Identity 95.9

- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10451
- gi No. 4587534
- % Identity 75.3
- Alignment Length 73
- Location of Alignment in SEQ ID NO 1320: from 1 to 73

- Alignment No. 10452
- gi No. 4589760
- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10453
- gi No. 4589760
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10454
- gi No. 463363
- % Identity 84.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10455
- gi No. 463363
- % Identity 85.5
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10456
- gi No. 463365
- % Identity 90
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10457
- gi No. 463365
- % Identity 90.8
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10458
- gi No. 463367
- % Identity 88.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10459
- gi No. 463367
- % Identity 89.5
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10460
- gi No. 463369
- % Identity 91.4
- Alignment Length 70

- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10461
- gi No. 463369
- % Identity 92.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10462
- gi No. 463371
- % Identity 87.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10463
- gi No. 463371
- % Identity 88.2
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10464
- gi No. 463373
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10465
- gi No. 463373
- % Identity 93.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10466
- gi No. 463375
- % Identity 91.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10467
- gi No. 463375
- % Identity 92.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10468
- gi No. 464989
- % Identity 78.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10469
- gi No. 464989
- % Identity 80.3
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10470
- gi No. 464990
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10471
- gi No. 464990
- % Identity 93.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10472
- gi No. 468272
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10473
- gi No. 468272
- % Identity 94.8
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77

- Alignment No. 10474
- gi No. 4737
- % Identity 95.7
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1320: from 1 to 47

- Alignment No. 10475
- gi No. 4737
- % Identity 95.7
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1320: from 77 to 123

- Alignment No. 10476
- gi No. 477437
- % Identity 76
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1320: from 3 to 27

- Alignment No. 10477
- gi No. 477437
- % Identity 76
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1320: from 79 to 103

- Alignment No. 10478
- gi No. 477630
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10479
- gi No. 477630
- % Identity 94.4
- Alignment Length 126
- Location of Alignment in SEQ ID NO 1320: from 21 to 146

- Alignment No. 10480
- gi No. 477815
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10481
- gi No. 477815
- % Identity 93.5
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77

- Alignment No. 10482
- gi No. 478811
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10483
- gi No. 478811
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10484
- gi No. 478811
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10485
- gi No. 478811
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10486
- gi No. 4809266
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10487
- gi No. 4809266
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10488
- gi No. 4809266
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10489
- gi No. 4809266
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10490
- gi No. 4809266
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10491

- gi No. 481477
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10492
- gi No. 481477
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10493
- gi No. 481477
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10494
- gi No. 481477
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10495
- gi No. 481477
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10496
- gi No. 481477
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10497
- gi No. 485427
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 1 to 70

- Alignment No. 10498
- gi No. 485427
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10499
- gi No. 485518
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10500
- gi No. 485518
- % Identity 98.7
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77

- Alignment No. 10501
- gi No. 49586

- % Identity 95.8
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1320: from 1 to 71

- Alignment No. 10502
- gi No. 49586
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10503
- gi No. 49586
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10504
- gi No. 510473
- % Identity 85.4
- Alignment Length 89
- Location of Alignment in SEQ ID NO 1320: from 1 to 89

- Alignment No. 10505
- gi No. 510473
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10506
- gi No. 510473
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10507
- gi No. 510473
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10508
- gi No. 510473
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10509
- gi No. 510473
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10510
- gi No. 510473
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10511
- gi No. 510473
- % Identity 95.9

- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10512
- gi No. 510473
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10513
- gi No. 510476
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10514
- gi No. 510476
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10515
- gi No. 5107695
- % Identity 85.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10516
- gi No. 5107695
- % Identity 86.8
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10517
- gi No. 539404
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10518
- gi No. 539404
- % Identity 85.2
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1320: from 1 to 87

- Alignment No. 10519
- gi No. 539935
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10520
- gi No. 539935
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10521
- gi No. 539935
- % Identity 95.9
- Alignment Length 146

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- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10522
- gi No. 539935
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10523
- gi No. 541546
- % Identity 97.4
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
- Alignment No. 10524
- gi No. 541546
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10525
- gi No. 541546
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10526
- gi No. 541546
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10527
- gi No. 541546
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10528
- gi No. 541953
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10529
- gi No. 541953
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10530
- gi No. 541954
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10531
- gi No. 541954
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10532
- gi No. 542395
- % Identity 97.9
- Alignment Length 48
- Location of Alignment in SEQ ID NO 1320: from 99 to 146
- Alignment No. 10533
- gi No. 542395
- % Identity 98.1
- Alignment Length 54
- Location of Alignment in SEQ ID NO 1320: from 23 to 76
- Alignment No. 10534
- gi No. 5441519
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10535
- gi No. 5441519
- % Identity 94.8
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
- Alignment No. 10536
- gi No. 552237
- % Identity 97.1
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1320: from 112 to 146
- Alignment No. 10537
- gi No. 552237
- % Identity 91.7
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1320: from 1 to 36
- Alignment No. 10538
- gi No. 552237
- % Identity 94.8
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 36 to 112
- Alignment No. 10539
- gi No. 5523967
- % Identity 88.2
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1320: from 1 to 85
- Alignment No. 10540
- gi No. 5523967
- % Identity 96.6
- Alignment Length 87
- Location of Alignment in SEQ ID NO 1320: from 60 to 146
- Alignment No. 10541
- gi No. 5523969
- % Identity 95.1
- Alignment Length 82
- Location of Alignment in SEQ ID NO 1320: from 65 to 146

- Alignment No. 10542
- gi No. 5523969
- % Identity 88.2
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1320: from 1 to 85

- Alignment No. 10543
- gi No. 5523969
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10544
- gi No. 5523971
- % Identity 88.2
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1320: from 1 to 85

- Alignment No. 10545
- gi No. 5523971
- % Identity 95.5
- Alignment Length 89
- Location of Alignment in SEQ ID NO 1320: from 58 to 146

- Alignment No. 10546
- gi No. 5523973
- % Identity 88.2
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1320: from 1 to 85

- Alignment No. 10547
- gi No. 5523973
- % Identity 87.6
- Alignment Length 121
- Location of Alignment in SEQ ID NO 1320: from 26 to 146

- Alignment No. 10548
- gi No. 5523975
- % Identity 95.9
- Alignment Length 73
- Location of Alignment in SEQ ID NO 1320: from 74 to 146

- Alignment No. 10549
- gi No. 5523975
- % Identity 88.2
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1320: from 1 to 85

- Alignment No. 10550
- gi No. 5523977
- % Identity 88.2
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1320: from 1 to 85

- Alignment No. 10551
- gi No. 5523977
- % Identity 95.6
- Alignment Length 114
- Location of Alignment in SEQ ID NO 1320: from 33 to 146

- Alignment No. 10552

- gi No. 5523979
- % Identity 88.2
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1320: from 1 to 85
- Alignment No. 10553
- gi No. 5523979
- % Identity 72.2
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1320: from 39 to 146
- Alignment No. 10554
- gi No. 5523979
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10555
- gi No. 5523981
- % Identity 88.2
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1320: from 1 to 85
- Alignment No. 10556
- gi No. 5523981
- % Identity 89.7
- Alignment Length 97
- Location of Alignment in SEQ ID NO 1320: from 50 to 146
- Alignment No. 10557
- gi No. 5523983
- % Identity 94.1
- Alignment Length 68
- Location of Alignment in SEQ ID NO 1320: from 79 to 146
- Alignment No. 10558
- gi No. 5523983
- % Identity 86.7
- Alignment Length 83
- Location of Alignment in SEQ ID NO 1320: from 3 to 85
- Alignment No. 10559
- gi No. 5523985
- % Identity 87.1
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1320: from 1 to 85
- Alignment No. 10560
- gi No. 5523985
- % Identity 94.9
- Alignment Length 118
- Location of Alignment in SEQ ID NO 1320: from 29 to 146
- Alignment No. 10561
- gi No. 5523987
- % Identity 88.2
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1320: from 1 to 85
- Alignment No. 10562
- gi No. 5523987

- % Identity 96.6
- Alignment Length 118
- Location of Alignment in SEQ ID NO 1320: from 29 to 146

- Alignment No. 10563
- gi No. 5531273
- % Identity 96.1
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77

- Alignment No. 10564
- gi No. 5531273
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10565
- gi No. 5531273
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10566
- gi No. 5531273
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10567
- gi No. 5531273
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10568
- gi No. 5531278
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10569
- gi No. 5531278
- % Identity 87.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1320: from 1 to 87

- Alignment No. 10570
- gi No. 5531281
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10571
- gi No. 5531281
- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10572
- gi No. 554564
- % Identity 93.2

- Alignment Length 73
- Location of Alignment in SEQ ID NO 1320: from 74 to 146

- Alignment No. 10573
- gi No. 554564
- % Identity 94.8
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77

- Alignment No. 10574
- gi No. 567767
- % Identity 88.2
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1320: from 1 to 85

- Alignment No. 10575
- gi No. 567767
- % Identity 84
- Alignment Length 100
- Location of Alignment in SEQ ID NO 1320: from 47 to 146

- Alignment No. 10576
- gi No. 567767
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10577
- gi No. 571519
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10578
- gi No. 571519
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10579
- gi No. 571519
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10580
- gi No. 571519
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10581
- gi No. 571519
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10582
- gi No. 571519
- % Identity 95.9
- Alignment Length 146

- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10583
- gi No. 576773
- % Identity 98.7
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
- Alignment No. 10584
- gi No. 576773
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10585
- gi No. 576773
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10586
- gi No. 576773
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10587
- gi No. 576773
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10588
- gi No. 576775
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10589
- gi No. 576775
- % Identity 87.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1320: from 1 to 87
- Alignment No. 10590
- gi No. 578545
- % Identity 89.3
- Alignment Length 75
- Location of Alignment in SEQ ID NO 1320: from 1 to 75
- Alignment No. 10591
- gi No. 578545
- % Identity 89
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10592
- gi No. 578545
- % Identity 89.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10593
- gi No. 578545
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10594
- gi No. 578545
- % Identity 84.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10595
- gi No. 578546
- % Identity 85.3
- Alignment Length 75
- Location of Alignment in SEQ ID NO 1320: from 1 to 75

- Alignment No. 10596
- gi No. 578546
- % Identity 87
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10597
- gi No. 578546
- % Identity 84.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10598
- gi No. 578546
- % Identity 87
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10599
- gi No. 578546
- % Identity 83.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10600
- gi No. 578549
- % Identity 81.3
- Alignment Length 75
- Location of Alignment in SEQ ID NO 1320: from 1 to 75

- Alignment No. 10601
- gi No. 578549
- % Identity 85.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10602
- gi No. 578549
- % Identity 84.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

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- Alignment No. 10603
- gi No. 578549
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10604
- gi No. 578551
- % Identity 89.3
- Alignment Length 75
- Location of Alignment in SEQ ID NO 1320: from 1 to 75

- Alignment No. 10605
- gi No. 578551
- % Identity 86.8
- Alignment Length 144
- Location of Alignment in SEQ ID NO 1320: from 3 to 146

- Alignment No. 10606
- gi No. 578551
- % Identity 88.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10607
- gi No. 578551
- % Identity 88.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10608
- gi No. 578551
- % Identity 88.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10609
- gi No. 600539
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10610
- gi No. 600539
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10611
- gi No. 602076
- % Identity 100
- Alignment Length 113
- Location of Alignment in SEQ ID NO 1320: from 1 to 113

- Alignment No. 10612
- gi No. 602076
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10613

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- gi No. 602076
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10614
- gi No. 602076
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10615
- gi No. 625174
- % Identity 86.7
- Alignment Length 90
- Location of Alignment in SEQ ID NO 1320: from 1 to 89

- Alignment No. 10616
- gi No. 625174
- % Identity 95.3
- Alignment Length 129
- Location of Alignment in SEQ ID NO 1320: from 18 to 146

- Alignment No. 10617
- gi No. 625174
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10618
- gi No. 625509
- % Identity 100
- Alignment Length 90
- Location of Alignment in SEQ ID NO 1320: from 57 to 146

- Alignment No. 10619
- gi No. 625509
- % Identity 97.7
- Alignment Length 129
- Location of Alignment in SEQ ID NO 1320: from 1 to 129

- Alignment No. 10620
- gi No. 625509
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10621
- gi No. 625509
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10622
- gi No. 630455
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10623
- gi No. 630455

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- % Identity 96.1
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77

- Alignment No. 10624
- gi No. 630479
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10625
- gi No. 630479
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10626
- gi No. 630479
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10627
- gi No. 630479
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10628
- gi No. 630479
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10629
- gi No. 70636
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10630
- gi No. 70636
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10631
- gi No. 70637
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10632
- gi No. 70637
- % Identity 95.9
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1320: from 1 to 74

- Alignment No. 10633
- gi No. 70639
- % Identity 97.4

- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10634
- gi No. 70639
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10635
- gi No. 70639
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10636
- gi No. 70639
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10637
- gi No. 70640
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10638
- gi No. 70640
- % Identity 97.4
- Alignment Length 78
- Location of Alignment in SEQ ID NO 1320: from 1 to 78
- Alignment No. 10639
- gi No. 70642
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10640
- gi No. 70642
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10641
- gi No. 70642
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10642
- gi No. 70642
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10643
- gi No. 70642
- % Identity 100
- Alignment Length 146

- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10644
- gi No. 70643
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10645
- gi No. 70643
- % Identity 100
- Alignment Length 81
- Location of Alignment in SEQ ID NO 1320: from 66 to 146
- Alignment No. 10646
- gi No. 70644
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10647
- gi No. 70644
- % Identity 100
- Alignment Length 99
- Location of Alignment in SEQ ID NO 1320: from 48 to 146
- Alignment No. 10648
- gi No. 70644
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10649
- gi No. 70644
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10650
- gi No. 70644
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10651
- gi No. 70644
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10652
- gi No. 70645
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10653
- gi No. 70645
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10654
- gi No. 70645
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10655
- gi No. 70645
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10656
- gi No. 70645
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10657
- gi No. 70646
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10658
- gi No. 70646
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10659
- gi No. 70647
- % Identity 93.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10660
- gi No. 70647
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10661
- gi No. 70647
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10662
- gi No. 70648
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10663
- gi No. 70648
- % Identity 93.5
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77

- Alignment No. 10664
- gi No. 70650
- % Identity 74.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10665
- gi No. 70650
- % Identity 76.3
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10666
- gi No. 70653
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10667
- gi No. 70653
- % Identity 92.3
- Alignment Length 78
- Location of Alignment in SEQ ID NO 1320: from 1 to 78

- Alignment No. 10668
- gi No. 70654
- % Identity 98.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10669
- gi No. 70654
- % Identity 97.4
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77

- Alignment No. 10670
- gi No. 70657
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10671
- gi No. 70657
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10672
- gi No. 70658
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10673
- gi No. 70658
- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10674

- gi No. 70659
- % Identity 96.9
- Alignment Length 65
- Location of Alignment in SEQ ID NO 1320: from 82 to 146

- Alignment No. 10675
- gi No. 70659
- % Identity 97.2
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1320: from 6 to 76

- Alignment No. 10676
- gi No. 70660
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10677
- gi No. 70660
- % Identity 93.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10678
- gi No. 726391
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10679
- gi No. 726391
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10680
- gi No. 726391
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10681
- gi No. 726391
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10682
- gi No. 726391
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10683
- gi No. 726391
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10684
- gi No. 726391

- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10685
- gi No. 726391
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10686
- gi No. 726391
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10687
- gi No. 726391
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10688
- gi No. 726391
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10689
- gi No. 82040
- % Identity 99.1
- Alignment Length 111
- Location of Alignment in SEQ ID NO 1320: from 36 to 146

- Alignment No. 10690
- gi No. 82040
- % Identity 100
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1320: from 1 to 112

- Alignment No. 10691
- gi No. 82040
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10692
- gi No. 82040
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10693
- gi No. 82284
- % Identity 100
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1320: from 1 to 56

- Alignment No. 10694
- gi No. 82284
- % Identity 100

- Alignment Length 56
- Location of Alignment in SEQ ID NO 1320: from 77 to 132
- Alignment No. 10695
- gi No. 82286
- % Identity 100
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1320: from 133 to 146
- Alignment No. 10696
- gi No. 82286
- % Identity 100
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1320: from 57 to 76
- Alignment No. 10697
- gi No. 82287
- % Identity 100
- Alignment Length 48
- Location of Alignment in SEQ ID NO 1320: from 1 to 48
- Alignment No. 10698
- gi No. 82287
- % Identity 100
- Alignment Length 48
- Location of Alignment in SEQ ID NO 1320: from 77 to 124
- Alignment No. 10699
- gi No. 82288
- % Identity 100
- Alignment Length 34
- Location of Alignment in SEQ ID NO 1320: from 113 to 146
- Alignment No. 10700
- gi No. 82288
- % Identity 100
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1320: from 37 to 76
- Alignment No. 10701
- gi No. 82426
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10702
- gi No. 82426
- % Identity 100
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1320: from 59 to 146
- Alignment No. 10703
- gi No. 82426
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10704
- gi No. 82512
- % Identity 98.7
- Alignment Length 77

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- Location of Alignment in SEQ ID NO 1320: from 1 to 77
- Alignment No. 10705
- gi No. 82512
- % Identity 100
- Alignment Length 106
- Location of Alignment in SEQ ID NO 1320: from 41 to 146
- Alignment No. 10706
- gi No. 82512
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10707
- gi No. 825728
- % Identity 96.8
- Alignment Length 31
- Location of Alignment in SEQ ID NO 1320: from 116 to 146
- Alignment No. 10708
- gi No. 825728
- % Identity 94.7
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1320: from 40 to 77
- Alignment No. 10709
- gi No. 82733
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10710
- gi No. 82733
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10711
- gi No. 82734
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10712
- gi No. 82734
- % Identity 100
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1320: from 35 to 146
- Alignment No. 10713
- gi No. 82734
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10714
- gi No. 82734
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10715
- gi No. 829173
- % Identity 93.1
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1320: from 89 to 146

- Alignment No. 10716
- gi No. 829173
- % Identity 90.9
- Alignment Length 66
- Location of Alignment in SEQ ID NO 1320: from 13 to 78

- Alignment No. 10717
- gi No. 83594
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10718
- gi No. 83594
- % Identity 87.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1320: from 1 to 87

- Alignment No. 10719
- gi No. 83596
- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10720
- gi No. 83596
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10721
- gi No. 83596
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10722
- gi No. 83596
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10723
- gi No. 83596
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10724
- gi No. 84151
- % Identity 93.5
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77

- Alignment No. 10725
- gi No. 84151
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10726
- gi No. 84151
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10727
- gi No. 84152
- % Identity 93.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10728
- gi No. 84152
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10729
- gi No. 84152
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10730
- gi No. 84152
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10731
- gi No. 84152
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10732
- gi No. 84336
- % Identity 94.2
- Alignment Length 52
- Location of Alignment in SEQ ID NO 1320: from 95 to 146

- Alignment No. 10733
- gi No. 84336
- % Identity 93.3
- Alignment Length 60
- Location of Alignment in SEQ ID NO 1320: from 19 to 78

- Alignment No. 10734
- gi No. 84337
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10735

- gi No. 84337
- % Identity 93.7
- Alignment Length 95
- Location of Alignment in SEQ ID NO 1320: from 1 to 95

- Alignment No. 10736
- gi No. 84478
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10737
- gi No. 84478
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10738
- gi No. 84478
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10739
- gi No. 84478
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10740
- gi No. 84478
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10741
- gi No. 84478
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10742
- gi No. 84478
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10743
- gi No. 84478
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10744
- gi No. 84478
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10745
- gi No. 84478

- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10746
- gi No. 84478
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10747
- gi No. 84834
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10748
- gi No. 84834
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10749
- gi No. 84834
- % Identity 96.7
- Alignment Length 92
- Location of Alignment in SEQ ID NO 1320: from 1 to 92

- Alignment No. 10750
- gi No. 84834
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1320: from 54 to 146

- Alignment No. 10751
- gi No. 85106
- % Identity 94.9
- Alignment Length 78
- Location of Alignment in SEQ ID NO 1320: from 1 to 78

- Alignment No. 10752
- gi No. 85106
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10753
- gi No. 85106
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10754
- gi No. 86473
- % Identity 96.2
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1320: from 121 to 146

- Alignment No. 10755
- gi No. 86473
- % Identity 93.8

- Alignment Length 32
- Location of Alignment in SEQ ID NO 1320: from 45 to 76

- Alignment No. 10756
- gi No. 86474
- % Identity 94.4
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1320: from 60 to 77

- Alignment No. 10757
- gi No. 870794
- % Identity 89.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10758
- gi No. 870794
- % Identity 75.5
- Alignment Length 149
- Location of Alignment in SEQ ID NO 1320: from 1 to 147

- Alignment No. 10759
- gi No. 870794
- % Identity 79.6
- Alignment Length 152
- Location of Alignment in SEQ ID NO 1320: from 1 to 145

- Alignment No. 10760
- gi No. 870794
- % Identity 70.5
- Alignment Length 167
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10761
- gi No. 89311
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10762
- gi No. 89311
- % Identity 95.8
- Alignment Length 96
- Location of Alignment in SEQ ID NO 1320: from 51 to 146

- Alignment No. 10763
- gi No. 89311
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10764
- gi No. 89311
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10765
- gi No. 899115
- % Identity 100
- Alignment Length 70

- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10766
- gi No. 899115
- % Identity 100
- Alignment Length 99
- Location of Alignment in SEQ ID NO 1320: from 1 to 99
- Alignment No. 10767
- gi No. 899608
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10768
- gi No. 899608
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10769
- gi No. 899608
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10770
- gi No. 899608
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10771
- gi No. 899608
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10772
- gi No. 902525
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10773
- gi No. 902525
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10774
- gi No. 902584
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10775
- gi No. 902584
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

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- Alignment No. 10776
- gi No. 902584
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10777
- gi No. 902584
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10778
- gi No. 902584
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10779
- gi No. 902584
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10780
- gi No. 902584
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10781
- gi No. 902586
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10782
- gi No. 902586
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10783
- gi No. 902586
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10784
- gi No. 902586
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10785
- gi No. 902586
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10786
- gi No. 91870
- % Identity 96
- Alignment Length 75
- Location of Alignment in SEQ ID NO 1320: from 72 to 146

- Alignment No. 10787
- gi No. 91870
- % Identity 93.9
- Alignment Length 98
- Location of Alignment in SEQ ID NO 1320: from 1 to 98

- Alignment No. 10788
- gi No. 91871
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10789
- gi No. 91871
- % Identity 94.8
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77

- Alignment No. 10790
- gi No. 9295
- % Identity 85.7
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1320: from 84 to 146

- Alignment No. 10791
- gi No. 9295
- % Identity 87
- Alignment Length 69
- Location of Alignment in SEQ ID NO 1320: from 8 to 76

- Alignment No. 10792
- gi No. 940395
- % Identity 88.9
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1320: from 1 to 108

- Alignment No. 10793
- gi No. 940395
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10794
- gi No. 940395
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10795
- gi No. 940395
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10796

- gi No. 940395
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10797
- gi No. 940395
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10798
- gi No. 940395
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10799
- gi No. 940395
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10800
- gi No. 967985
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10801
- gi No. 967985
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10802
- gi No. 99469
- % Identity 100
- Alignment Length 33
- Location of Alignment in SEQ ID NO 1320: from 114 to 146

- Alignment No. 10803
- gi No. 99469
- % Identity 100
- Alignment Length 42
- Location of Alignment in SEQ ID NO 1320: from 38 to 79

- Alignment No. 10804
- gi No. 99771
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10805
- gi No. 99771
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10806
- gi No. 99772

- ```
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10807
- gi No. 99772
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10808
- gi No. 99975
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10809
- gi No. 99975
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
```

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1321
- Ceres seq\_id 1500056
- Location of start within SEQ ID NO 1319: at 629 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 10810
- Ubiquitin family
- Location within SEQ ID NO 1321: from 1 to 70 aa.

#### (D) Related Amino Acid Sequences

- ```
- Alignment No. 10811
- gi No. 100490
- % Identity 100
- Alignment Length 137
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10812
- gi No. 100490
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10813
- gi No. 100490
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10814
- gi No. 100524
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10815
- gi No. 100524
- % Identity 100
```

- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10816
- gi No. 100524
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10817
- gi No. 100524
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10818
- gi No. 100524
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10819
- gi No. 100525
- % Identity 100
- Alignment Length 106
- Location of Alignment in SEQ ID NO 1321: from 1 to 30
- Alignment No. 10820
- gi No. 100525
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10821
- gi No. 100525
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10822
- gi No. 100525
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10823
- gi No. 100598
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10824
- gi No. 100599
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10825
- gi No. 100812
- % Identity 100
- Alignment Length 70

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- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10826
- gi No. 100934
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10827
- gi No. 100934
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10828
- gi No. 100934
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10829
- gi No. 100934
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10830
- gi No. 100934
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10831
- gi No. 100934
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10832
- gi No. 100981
- % Identity 100
- Alignment Length 34
- Location of Alignment in SEQ ID NO 1321: from 37 to 70
- Alignment No. 10833
- gi No. 102062
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10834
- gi No. 102278
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10835
- gi No. 102278
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10836
- gi No. 102278
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10837
- gi No. 102278
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10838
- gi No. 102278
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10839
- gi No. 102278
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10840
- gi No. 102279
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10841
- gi No. 102279
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10842
- gi No. 102280
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10843
- gi No. 102280
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10844
- gi No. 102280
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10845
- gi No. 102280
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10846
- gi No. 102281
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10847
- gi No. 102281
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10848
- gi No. 102281
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10849
- gi No. 102281
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10850
- gi No. 102389
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10851
- gi No. 102389
- % Identity 85.2
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1321: from 1 to 11

- Alignment No. 10852
- gi No. 103436
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10853
- gi No. 1044940
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10854
- gi No. 104829
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10855
- gi No. 104829
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10856

- gi No. 1050930
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10857
- gi No. 1050930
- % Identity 95
- Alignment Length 100
- Location of Alignment in SEQ ID NO 1321: from 1 to 24

- Alignment No. 10858
- gi No. 10673
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10859
- gi No. 10673
- % Identity 87.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1321: from 1 to 11

- Alignment No. 10860
- gi No. 1070590
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10861
- gi No. 1070590
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10862
- gi No. 1070591
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10863
- gi No. 1070591
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10864
- gi No. 1070591
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10865
- gi No. 1070591
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10866
- gi No. 1070591

- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10867
- gi No. 1070591
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10868
- gi No. 1070591
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10869
- gi No. 1070591
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10870
- gi No. 1076678
- % Identity 79.2
- Alignment Length 96
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10871
- gi No. 1076708
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10872
- gi No. 1076708
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10873
- gi No. 1076708
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10874
- gi No. 1078777
- % Identity 87.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10875
- gi No. 1078813
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10876
- gi No. 1078813
- % Identity 95.9

- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10877
- gi No. 1083758
- % Identity 88
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1321: from 1 to 32
- Alignment No. 10878
- gi No. 1083758
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10879
- gi No. 1083758
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10880
- gi No. 1083758
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10881
- gi No. 1083758
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10882
- gi No. 1083758
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10883
- gi No. 1083758
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10884
- gi No. 1083758
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10885
- gi No. 1083758
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10886
- gi No. 1083758
- % Identity 95.9
- Alignment Length 146

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- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10887
- gi No. 1101011
- % Identity 87.3
- Alignment Length 79
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10888
- gi No. 1101011
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10889
- gi No. 1101011
- % Identity 84.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10890
- gi No. 1101011
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10891
- gi No. 1101011
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10892
- gi No. 1101011
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10893
- gi No. 1101011
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10894
- gi No. 1101011
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10895
- gi No. 1101011
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10896
- gi No. 1101011
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

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- Alignment No. 10897
- gi No. 1101013
- % Identity 85
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1321: from 7 to 46

- Alignment No. 10898
- gi No. 1101015
- % Identity 85
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1321: from 7 to 46

- Alignment No. 10899
- gi No. 1101019
- % Identity 80
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1321: from 7 to 46

- Alignment No. 10900
- gi No. 1101021
- % Identity 84.4
- Alignment Length 64
- Location of Alignment in SEQ ID NO 1321: from 7 to 70

- Alignment No. 10901
- gi No. 1101021
- % Identity 86.2
- Alignment Length 116
- Location of Alignment in SEQ ID NO 1321: from 1 to 46

- Alignment No. 10902
- gi No. 1101023
- % Identity 87.9
- Alignment Length 33
- Location of Alignment in SEQ ID NO 1321: from 38 to 70

- Alignment No. 10903
- gi No. 1101023
- % Identity 92
- Alignment Length 50
- Location of Alignment in SEQ ID NO 1321: from 1 to 11

- Alignment No. 10904
- gi No. 1107481
- % Identity 97.9
- Alignment Length 96
- Location of Alignment in SEQ ID NO 1321: from 1 to 20

- Alignment No. 10905
- gi No. 1107481
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10906
- gi No. 1143188
- % Identity 94.5
- Alignment Length 73
- Location of Alignment in SEQ ID NO 1321: from 1 to 73

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- Alignment No. 10907
- gi No. 1143188
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10908
- gi No. 1143188
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10909
- gi No. 1167510
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10910
- gi No. 1167510
- % Identity 91.3
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1321: from 1 to 27

- Alignment No. 10911
- gi No. 1174858
- % Identity 74.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10912
- gi No. 1174859
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10913
- gi No. 1174860
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10914
- gi No. 1174861
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10915
- gi No. 1184755
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10916
- gi No. 1197093
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10917

- gi No. 1197093
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10918
- gi No. 1197093
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10919
- gi No. 1304128
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10920
- gi No. 1304128
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10921
- gi No. 1304128
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10922
- gi No. 1304128
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10923
- gi No. 1304128
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10924
- gi No. 1304128
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10925
- gi No. 1304128
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10926
- gi No. 1304357
- % Identity 81.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10927
- gi No. 1321735

- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10928
- gi No. 1321735
- % Identity 95.7
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1321: from 1 to 63

- Alignment No. 10929
- gi No. 1326021
- % Identity 96.3
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1321: from 44 to 70

- Alignment No. 10930
- gi No. 1326022
- % Identity 97.2
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10931
- gi No. 1326022
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10932
- gi No. 1332579
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10933
- gi No. 1332579
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10934
- gi No. 1332579
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10935
- gi No. 1332579
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10936
- gi No. 1332579
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10937
- gi No. 1332579
- % Identity 98.6

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- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10938
- gi No. 1332579
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10939
- gi No. 1332579
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10940
- gi No. 1332579
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10941
- gi No. 1351348
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10942
- gi No. 1351349
- % Identity 90
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10943
- gi No. 1353755
- % Identity 95.2
- Alignment Length 105
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10944
- gi No. 1353757
- % Identity 94.2
- Alignment Length 69
- Location of Alignment in SEQ ID NO 1321: from 2 to 70

- Alignment No. 10945
- gi No. 1353757
- % Identity 94.2
- Alignment Length 121
- Location of Alignment in SEQ ID NO 1321: from 1 to 46

- Alignment No. 10946
- gi No. 1362008
- % Identity 92.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10947
- gi No. 1362008
- % Identity 92.5
- Alignment Length 146

- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10948
- gi No. 1362008
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10949
- gi No. 1362008
- % Identity 92.5
- Alignment Length 159
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10950
- gi No. 1362009
- % Identity 79.7
- Alignment Length 148
- Location of Alignment in SEQ ID NO 1321: from 1 to 72
- Alignment No. 10951
- gi No. 1362010
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10952
- gi No. 1362010
- % Identity 88.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10953
- gi No. 1362010
- % Identity 92.5
- Alignment Length 147
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10954
- gi No. 1362012
- % Identity 89.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10955
- gi No. 1362012
- % Identity 76.2
- Alignment Length 149
- Location of Alignment in SEQ ID NO 1321: from 1 to 71
- Alignment No. 10956
- gi No. 1362012
- % Identity 79.6
- Alignment Length 152
- Location of Alignment in SEQ ID NO 1321: from 1 to 69
- Alignment No. 10957
- gi No. 1362012
- % Identity 71.1
- Alignment Length 167
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

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- Alignment No. 10958
- gi No. 136665
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10959
- gi No. 136666
- % Identity 98.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10960
- gi No. 136667
- % Identity 98.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10961
- gi No. 136668
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10962
- gi No. 136669
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10963
- gi No. 136670
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10964
- gi No. 136671
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10965
- gi No. 136672
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10966
- gi No. 136673
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10967
- gi No. 136674
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

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- Alignment No. 10968
 - gi No. 136675
 - % Identity 94.3
 - Alignment Length 70
 - Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10969
 - gi No. 136676
 - % Identity 94.3
 - Alignment Length 70
 - Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10970
 - gi No. 136677
 - % Identity 97.1
 - Alignment Length 70
 - Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10971
 - gi No. 136678
 - % Identity 97.1
 - Alignment Length 70
 - Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10972
 - gi No. 1421797
 - % Identity 95.7
 - Alignment Length 70
 - Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10973
 - gi No. 1480012
 - % Identity 96.3
 - Alignment Length 54
 - Location of Alignment in SEQ ID NO 1321: from 17 to 70
- Alignment No. 10974
 - gi No. 156480
 - % Identity 94.6
 - Alignment Length 37
 - Location of Alignment in SEQ ID NO 1321: from 1 to 37
- Alignment No. 10975
 - gi No. 158759
 - % Identity 94.3
 - Alignment Length 70
 - Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10976
 - gi No. 158763
 - % Identity 94.3
 - Alignment Length 70
 - Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10977
 - gi No. 158765
 - % Identity 91.4
 - Alignment Length 70
 - Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10978

- gi No. 158767
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10979
- gi No. 158769
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10980
- gi No. 158771
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10981
- gi No. 161281
- % Identity 94.4
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1321: from 1 to 71

- Alignment No. 10982
- gi No. 163575
- % Identity 96.3
- Alignment Length 81
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10983
- gi No. 163575
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10984
- gi No. 166336
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10985
- gi No. 166336
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10986
- gi No. 166336
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10987
- gi No. 166336
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10988
- gi No. 166336

- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10989
- gi No. 1666175
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10990
- gi No. 1675359
- % Identity 92.7
- Alignment Length 41
- Location of Alignment in SEQ ID NO 1321: from 1 to 41

- Alignment No. 10991
- gi No. 167935
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10992
- gi No. 167935
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10993
- gi No. 167935
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10994
- gi No. 167935
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10995
- gi No. 167941
- % Identity 92.8
- Alignment Length 69
- Location of Alignment in SEQ ID NO 1321: from 2 to 70

- Alignment No. 10996
- gi No. 167945
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10997
- gi No. 167945
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10998
- gi No. 167947
- % Identity 94.5

- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10999
- gi No. 167947
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11000
- gi No. 167947
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11001
- gi No. 167947
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11002
- gi No. 167947
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11003
- gi No. 167947
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11004
- gi No. 167949
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11005
- gi No. 167949
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11006
- gi No. 167949
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11007
- gi No. 167949
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11008
- gi No. 1684855
- % Identity 81.7
- Alignment Length 131

- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11009
- gi No. 1684855
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11010
- gi No. 1684855
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11011
- gi No. 1684855
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11012
- gi No. 1684857
- % Identity 100
- Alignment Length 132
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11013
- gi No. 1684857
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11014
- gi No. 170352
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11015
- gi No. 170352
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11016
- gi No. 170352
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11017
- gi No. 170352
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11018
- gi No. 170352
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

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- Alignment No. 11019
- gi No. 170354
- % Identity 100
- Alignment Length 142
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11020
- gi No. 170354
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11021
- gi No. 170354
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11022
- gi No. 170354
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11023
- gi No. 1762374
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11024
- gi No. 1762935
- % Identity 98.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11025
- gi No. 1763015
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11026
- gi No. 1771780
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11027
- gi No. 1778712
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11028
- gi No. 1778712
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

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- Alignment No. 11029
- gi No. 1778712
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11030
- gi No. 1778712
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11031
- gi No. 1800281
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11032
- gi No. 1800281
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11033
- gi No. 1800281
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11034
- gi No. 1800281
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11035
- gi No. 1805696
- % Identity 95.2
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1321: from 8 to 70

- Alignment No. 11036
- gi No. 1805696
- % Identity 95.5
- Alignment Length 134
- Location of Alignment in SEQ ID NO 1321: from 1 to 65

- Alignment No. 11037
- gi No. 1839584
- % Identity 100
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1321: from 1 to 38

- Alignment No. 11038
- gi No. 1841849
- % Identity 100
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1321: from 36 to 70

- Alignment No. 11039

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- gi No. 1841849
- % Identity 100
- Alignment Length 57
- Location of Alignment in SEQ ID NO 1321: from 1 to 16

- Alignment No. 11040
- gi No. 208558
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11041
- gi No. 208560
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11042
- gi No. 208562
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11043
- gi No. 208564
- % Identity 91.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11044
- gi No. 208566
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11045
- gi No. 208568
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11046
- gi No. 208891
- % Identity 96
- Alignment Length 75
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11047
- gi No. 208891
- % Identity 93.9
- Alignment Length 98
- Location of Alignment in SEQ ID NO 1321: from 1 to 22

- Alignment No. 11048
- gi No. 209603
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11049
- gi No. 2118958

- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11050
- gi No. 2118958
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11051
- gi No. 2118958
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11052
- gi No. 2118958
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11053
- gi No. 2118959
- % Identity 85.7
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1321: from 1 to 36

- Alignment No. 11054
- gi No. 2118959
- % Identity 84.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11055
- gi No. 2118959
- % Identity 83.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11056
- gi No. 2118960
- % Identity 96.5
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11057
- gi No. 2118960
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11058
- gi No. 2118961
- % Identity 94.6
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11059
- gi No. 2118961
- % Identity 95.2

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- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11060
- gi No. 2118962
- % Identity 95.9
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11061
- gi No. 2118962
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11062
- gi No. 2118963
- % Identity 91
- Alignment Length 111
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11063
- gi No. 2118964
- % Identity 96.4
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11064
- gi No. 2118964
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11065
- gi No. 2118964
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11066
- gi No. 2118965
- % Identity 96.3
- Alignment Length 81
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11067
- gi No. 2118965
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11068
- gi No. 2118965
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11069
- gi No. 2129452
- % Identity 95.9
- Alignment Length 146

- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11070
- gi No. 2129452
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11071
- gi No. 2129452
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11072
- gi No. 2129452
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11073
- gi No. 2129452
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11074
- gi No. 2133278
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11075
- gi No. 2133549
- % Identity 96.3
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1321: from 44 to 70
- Alignment No. 11076
- gi No. 2133549
- % Identity 96
- Alignment Length 50
- Location of Alignment in SEQ ID NO 1321: from 21 to 70
- Alignment No. 11077
- gi No. 2133549
- % Identity 96.3
- Alignment Length 81
- Location of Alignment in SEQ ID NO 1321: from 1 to 48
- Alignment No. 11078
- gi No. 2144011
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11079
- gi No. 2144275
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

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- Alignment No. 11080
- gi No. 2144734
- % Identity 87.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1321: from 1 to 11

- Alignment No. 11081
- gi No. 2144734
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11082
- gi No. 2144734
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11083
- gi No. 2144734
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11084
- gi No. 2149467
- % Identity 87.7
- Alignment Length 83
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11085
- gi No. 2209091
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11086
- gi No. 223061
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11087
- gi No. 224321
- % Identity 97.2
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11088
- gi No. 224321
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11089
- gi No. 225317
- % Identity 89.6
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1321: from 1 to 77

- Alignment No. 11090
- gi No. 225319
- % Identity 89.6
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1321: from 1 to 77

- Alignment No. 11091
- gi No. 225320
- % Identity 87
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1321: from 1 to 77

- Alignment No. 11092
- gi No. 2281952
- % Identity 95.2
- Alignment Length 62
- Location of Alignment in SEQ ID NO 1321: from 8 to 69

- Alignment No. 11093
- gi No. 2281954
- % Identity 93.5
- Alignment Length 62
- Location of Alignment in SEQ ID NO 1321: from 8 to 69

- Alignment No. 11094
- gi No. 2281955
- % Identity 88.9
- Alignment Length 45
- Location of Alignment in SEQ ID NO 1321: from 8 to 52

- Alignment No. 11095
- gi No. 2281959
- % Identity 90.6
- Alignment Length 64
- Location of Alignment in SEQ ID NO 1321: from 7 to 70

- Alignment No. 11096
- gi No. 2330875
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11097
- gi No. 2350864
- % Identity 75.9
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1321: from 6 to 63

- Alignment No. 11098
- gi No. 2408009
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11099
- gi No. 2408009
- % Identity 87.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1321: from 1 to 11

- Alignment No. 11100

- gi No. 2437825
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11101
- gi No. 2437825
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11102
- gi No. 2437825
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11103
- gi No. 247308
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11104
- gi No. 248865
- % Identity 95
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1321: from 1 to 20

- Alignment No. 11105
- gi No. 2558539
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11106
- gi No. 2627129
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11107
- gi No. 2627129
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11108
- gi No. 2627129
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11109
- gi No. 2627129
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11110
- gi No. 2627129

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- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11111
- gi No. 2627129
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11112
- gi No. 2627129
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11113
- gi No. 2627131
- % Identity 89.8
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1321: from 1 to 32

- Alignment No. 11114
- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11115
- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11116
- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11117
- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11118
- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11119
- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11120
- gi No. 2627131
- % Identity 95.9

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- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11121
- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11122
- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11123
- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11124
- gi No. 2627133
- % Identity 89.8
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1321: from 1 to 32

- Alignment No. 11125
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11126
- gi No. 2627133
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11127
- gi No. 2627133
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11128
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11129
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11130
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146

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- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11131
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11132
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11133
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11134
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11135
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11136
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11137
- gi No. 2641213
- % Identity 98.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11138
- gi No. 2641213
- % Identity 98.6
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1321: from 1 to 63
- Alignment No. 11139
- gi No. 2654141
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11140
- gi No. 2654141
- % Identity 91.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

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- Alignment No. 11141
- gi No. 2654141
- % Identity 89
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11142
- gi No. 2654141
- % Identity 89.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11143
- gi No. 2707837
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11144
- gi No. 2707837
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11145
- gi No. 2707837
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11146
- gi No. 2739333
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11147
- gi No. 2739333
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11148
- gi No. 2739333
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11149
- gi No. 2760345
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11150
- gi No. 2760345
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11151
- gi No. 2760345
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11152
- gi No. 2760347
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11153
- gi No. 2760347
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11154
- gi No. 2760347
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11155
- gi No. 2760347
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11156
- gi No. 2760347
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11157
- gi No. 2760349
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11158
- gi No. 2760349
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11159
- gi No. 2760349
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11160
- gi No. 2760349
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11161

- gi No. 279635
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11162
- gi No. 279636
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11163
- gi No. 280386
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11164
- gi No. 281276
- % Identity 90
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1321: from 1 to 20

- Alignment No. 11165
- gi No. 283496
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11166
- gi No. 283496
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11167
- gi No. 283496
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11168
- gi No. 283496
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11169
- gi No. 2894304
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11170
- gi No. 2894304
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11171
- gi No. 2894304

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- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11172
- gi No. 2894306
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11173
- gi No. 2894308
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11174
- gi No. 2894308
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11175
- gi No. 2894308
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11176
- gi No. 2894308
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11177
- gi No. 2995277
- % Identity 100
- Alignment Length 23
- Location of Alignment in SEQ ID NO 1321: from 48 to 70

- Alignment No. 11178
- gi No. 2995949
- % Identity 100
- Alignment Length 104
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11179
- gi No. 3047314
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11180
- gi No. 3047314
- % Identity 87.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1321: from 1 to 11

- Alignment No. 11181
- gi No. 3047316
- % Identity 97.1

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- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11182
- gi No. 3047318
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11183
- gi No. 3047318
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11184
- gi No. 3047318
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11185
- gi No. 3047318
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11186
- gi No. 3091264
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11187
- gi No. 3091264
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11188
- gi No. 3091264
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11189
- gi No. 3126967
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11190
- gi No. 3126967
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11191
- gi No. 3126967
- % Identity 100
- Alignment Length 146

- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11192
- gi No. 3126967
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11193
- gi No. 3126967
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11194
- gi No. 3152950
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11195
- gi No. 3158372
- % Identity 100
- Alignment Length 98
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11196
- gi No. 3158372
- % Identity 99.1
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1321: from 1 to 33
- Alignment No. 11197
- gi No. 320608
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11198
- gi No. 320608
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11199
- gi No. 320608
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11200
- gi No. 322750
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11201
- gi No. 323071
- % Identity 84.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

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- Alignment No. 11202
- gi No. 323157
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11203
- gi No. 323157
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11204
- gi No. 323157
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11205
- gi No. 323157
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11206
- gi No. 323157
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11207
- gi No. 323208
- % Identity 82.5
- Alignment Length 144
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11208
- gi No. 323230
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11209
- gi No. 3265058
- % Identity 98.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11210
- gi No. 3319208
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11211
- gi No. 3335355
- % Identity 100
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1321: from 56 to 70

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- Alignment No. 11212
- gi No. 3335355
- % Identity 97.7
- Alignment Length 129
- Location of Alignment in SEQ ID NO 1321: from 1 to 53

- Alignment No. 11213
- gi No. 3335355
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11214
- gi No. 3335355
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11215
- gi No. 340062
- % Identity 95.5
- Alignment Length 66
- Location of Alignment in SEQ ID NO 1321: from 5 to 70

- Alignment No. 11216
- gi No. 3452083
- % Identity 97.9
- Alignment Length 48
- Location of Alignment in SEQ ID NO 1321: from 23 to 70

- Alignment No. 11217
- gi No. 3452083
- % Identity 96.4
- Alignment Length 83
- Location of Alignment in SEQ ID NO 1321: from 1 to 29

- Alignment No. 11218
- gi No. 348148
- % Identity 96.3
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1321: from 44 to 70

- Alignment No. 11219
- gi No. 348148
- % Identity 96.3
- Alignment Length 81
- Location of Alignment in SEQ ID NO 1321: from 1 to 48

- Alignment No. 11220
- gi No. 348149
- % Identity 96
- Alignment Length 50
- Location of Alignment in SEQ ID NO 1321: from 21 to 70

- Alignment No. 11221
- gi No. 3603456
- % Identity 100
- Alignment Length 106
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11222

- gi No. 3603456
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11223
- gi No. 3603456
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11224
- gi No. 3687425
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11225
- gi No. 3687425
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11226
- gi No. 3738185
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11227
- gi No. 3738185
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11228
- gi No. 3738185
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11229
- gi No. 3738185
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11230
- gi No. 3776536
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11231
- gi No. 3776536
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11232
- gi No. 3776536

- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11233
- gi No. 3776536
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11234
- gi No. 3776536
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11235
- gi No. 3776536
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11236
- gi No. 3776536
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11237
- gi No. 3789940
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11238
- gi No. 3789940
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11239
- gi No. 3789940
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11240
- gi No. 3789942
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11241
- gi No. 3789942
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11242
- gi No. 3789942
- % Identity 98.6

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- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11243
- gi No. 3789942
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11244
- gi No. 3822277
- % Identity 75.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11245
- gi No. 385076
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11246
- gi No. 3882081
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11247
- gi No. 3882081
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11248
- gi No. 3885463
- % Identity 94
- Alignment Length 67
- Location of Alignment in SEQ ID NO 1321: from 4 to 70

- Alignment No. 11249
- gi No. 3892189
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11250
- gi No. 3892189
- % Identity 84.1
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1321: from 1 to 11

- Alignment No. 11251
- gi No. 402242
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11252
- gi No. 4049712
- % Identity 85.7
- Alignment Length 70

- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11253
- gi No. 4102845
- % Identity 86.2
- Alignment Length 65
- Location of Alignment in SEQ ID NO 1321: from 6 to 70
- Alignment No. 11254
- gi No. 4105408
- % Identity 95.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11255
- gi No. 4105408
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11256
- gi No. 4105408
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11257
- gi No. 4115337
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11258
- gi No. 4115337
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11259
- gi No. 4115337
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11260
- gi No. 4115337
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11261
- gi No. 4115337
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11262
- gi No. 4150898
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11263
- gi No. 4150898
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11264
- gi No. 4150898
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11265
- gi No. 4150912
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11266
- gi No. 4150912
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11267
- gi No. 4150912
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11268
- gi No. 4150912
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11269
- gi No. 4150914
- % Identity 95.7
- Alignment Length 140
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11270
- gi No. 4151082
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11271
- gi No. 418854
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11272
- gi No. 418854
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

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- Alignment No. 11273
- gi No. 418854
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11274
- gi No. 418854
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11275
- gi No. 418854
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11276
- gi No. 421735
- % Identity 94.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 1321: from 1 to 19

- Alignment No. 11277
- gi No. 421867
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11278
- gi No. 421929
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11279
- gi No. 421929
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11280
- gi No. 421929
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11281
- gi No. 421929
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11282
- gi No. 421929
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11283

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- gi No. 421929
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11284
- gi No. 422248
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11285
- gi No. 422248
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11286
- gi No. 422248
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11287
- gi No. 422248
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11288
- gi No. 422269
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11289
- gi No. 422270
- % Identity 90
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11290
- gi No. 422271
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11291
- gi No. 433970
- % Identity 95.5
- Alignment Length 111
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11292
- gi No. 433970
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11293
- gi No. 433970

- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11294
- gi No. 433970
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11295
- gi No. 433970
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11296
- gi No. 444791
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11297
- gi No. 444791
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11298
- gi No. 444791
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11299
- gi No. 4506713
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11300
- gi No. 4507761
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11301
- gi No. 4510359
- % Identity 100
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1321: from 36 to 70

- Alignment No. 11302
- gi No. 456779
- % Identity 92
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1321: from 1 to 25

- Alignment No. 11303
- gi No. 4586594
- % Identity 100

- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11304
- gi No. 4586594
- % Identity 100
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1321: from 1 to 32

- Alignment No. 11305
- gi No. 4587232
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11306
- gi No. 4587234
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11307
- gi No. 4587236
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11308
- gi No. 4587236
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11309
- gi No. 4587236
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11310
- gi No. 4587236
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11311
- gi No. 4587236
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11312
- gi No. 4587236
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11313
- gi No. 4587236
- % Identity 95.9
- Alignment Length 146

- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11314
- gi No. 4587236
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11315
- gi No. 4587236
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11316
- gi No. 4587236
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11317
- gi No. 4587236
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11318
- gi No. 4589760
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11319
- gi No. 463363
- % Identity 84.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11320
- gi No. 463365
- % Identity 90
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11321
- gi No. 463367
- % Identity 88.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11322
- gi No. 463369
- % Identity 91.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11323
- gi No. 463371
- % Identity 87.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11324
- gi No. 463373
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11325
- gi No. 463375
- % Identity 91.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11326
- gi No. 464989
- % Identity 78.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11327
- gi No. 464990
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11328
- gi No. 468272
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11329
- gi No. 4737
- % Identity 95.7
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1321: from 1 to 47

- Alignment No. 11330
- gi No. 477437
- % Identity 76
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1321: from 3 to 27

- Alignment No. 11331
- gi No. 477630
- % Identity 94.4
- Alignment Length 126
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11332
- gi No. 477815
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11333
- gi No. 478811
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

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- Alignment No. 11334
- gi No. 478811
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11335
- gi No. 478811
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11336
- gi No. 4809266
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11337
- gi No. 4809266
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11338
- gi No. 4809266
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11339
- gi No. 4809266
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11340
- gi No. 481477
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11341
- gi No. 481477
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11342
- gi No. 481477
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11343
- gi No. 481477
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11344

- gi No. 481477
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11345
- gi No. 485427
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11346
- gi No. 485518
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11347
- gi No. 49586
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11348
- gi No. 49586
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11349
- gi No. 510473
- % Identity 85.4
- Alignment Length 89
- Location of Alignment in SEQ ID NO 1321: from 1 to 13

- Alignment No. 11350
- gi No. 510473
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11351
- gi No. 510473
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11352
- gi No. 510473
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11353
- gi No. 510473
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11354
- gi No. 510473

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- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11355
- gi No. 510473
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11356
- gi No. 510473
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11357
- gi No. 510473
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11358
- gi No. 510476
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11359
- gi No. 5107695
- % Identity 85.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11360
- gi No. 539404
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11361
- gi No. 539404
- % Identity 85.2
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1321: from 1 to 11

- Alignment No. 11362
- gi No. 539935
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11363
- gi No. 539935
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11364
- gi No. 539935
- % Identity 95.9

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- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11365
- gi No. 541546
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11366
- gi No. 541546
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11367
- gi No. 541546
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11368
- gi No. 541546
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11369
- gi No. 541953
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11370
- gi No. 541954
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11371
- gi No. 542395
- % Identity 97.9
- Alignment Length 48
- Location of Alignment in SEQ ID NO 1321: from 23 to 70
  
- Alignment No. 11372
- gi No. 5441519
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11373
- gi No. 552237
- % Identity 97.1
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1321: from 36 to 70
  
- Alignment No. 11374
- gi No. 552237
- % Identity 94.8
- Alignment Length 77

- Location of Alignment in SEQ ID NO 1321: from 1 to 36
- Alignment No. 11375
- gi No. 5523967
- % Identity 96.6
- Alignment Length 87
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11376
- gi No. 5523969
- % Identity 95.1
- Alignment Length 82
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11377
- gi No. 5523969
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11378
- gi No. 5523971
- % Identity 95.5
- Alignment Length 89
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11379
- gi No. 5523973
- % Identity 87.6
- Alignment Length 121
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11380
- gi No. 5523975
- % Identity 95.9
- Alignment Length 73
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11381
- gi No. 5523977
- % Identity 95.6
- Alignment Length 114
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11382
- gi No. 5523979
- % Identity 72.2
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11383
- gi No. 5523979
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11384
- gi No. 5523981
- % Identity 89.7
- Alignment Length 97
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11385
- gi No. 5523983
- % Identity 94.1
- Alignment Length 68
- Location of Alignment in SEQ ID NO 1321: from 3 to 70
  
- Alignment No. 11386
- gi No. 5523985
- % Identity 94.9
- Alignment Length 118
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11387
- gi No. 5523987
- % Identity 96.6
- Alignment Length 118
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11388
- gi No. 5531273
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11389
- gi No. 5531273
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11390
- gi No. 5531273
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11391
- gi No. 5531273
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11392
- gi No. 5531278
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11393
- gi No. 5531278
- % Identity 87.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1321: from 1 to 11
  
- Alignment No. 11394
- gi No. 5531281
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11395
- gi No. 554564
- % Identity 93.2
- Alignment Length 73
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11396
- gi No. 567767
- % Identity 84
- Alignment Length 100
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11397
- gi No. 567767
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11398
- gi No. 571519
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11399
- gi No. 571519
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11400
- gi No. 571519
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11401
- gi No. 571519
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11402
- gi No. 571519
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11403
- gi No. 576773
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11404
- gi No. 576773
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11405

- gi No. 576773
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11406
- gi No. 576773
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11407
- gi No. 576775
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11408
- gi No. 576775
- % Identity 87.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1321: from 1 to 11
  
- Alignment No. 11409
- gi No. 578545
- % Identity 89
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11410
- gi No. 578545
- % Identity 84.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11411
- gi No. 578545
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11412
- gi No. 578545
- % Identity 89.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11413
- gi No. 578546
- % Identity 87
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11414
- gi No. 578546
- % Identity 83.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
  
- Alignment No. 11415
- gi No. 578546

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- % Identity 84.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11416
- gi No. 578546
- % Identity 87
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11417
- gi No. 578549
- % Identity 85.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11418
- gi No. 578549
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11419
- gi No. 578549
- % Identity 84.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11420
- gi No. 578551
- % Identity 86.8
- Alignment Length 144
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11421
- gi No. 578551
- % Identity 88.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11422
- gi No. 578551
- % Identity 88.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11423
- gi No. 578551
- % Identity 88.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11424
- gi No. 600539
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11425
- gi No. 602076
- % Identity 100

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- Alignment Length 113
- Location of Alignment in SEQ ID NO 1321: from 1 to 37

- Alignment No. 11426
- gi No. 602076
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11427
- gi No. 602076
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11428
- gi No. 602076
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11429
- gi No. 625174
- % Identity 86.7
- Alignment Length 90
- Location of Alignment in SEQ ID NO 1321: from 1 to 13

- Alignment No. 11430
- gi No. 625174
- % Identity 95.3
- Alignment Length 129
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11431
- gi No. 625174
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11432
- gi No. 625509
- % Identity 100
- Alignment Length 90
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11433
- gi No. 625509
- % Identity 97.7
- Alignment Length 129
- Location of Alignment in SEQ ID NO 1321: from 1 to 53

- Alignment No. 11434
- gi No. 625509
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11435
- gi No. 625509
- % Identity 98.6
- Alignment Length 146

- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11436
- gi No. 630455
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11437
- gi No. 630479
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11438
- gi No. 630479
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11439
- gi No. 630479
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11440
- gi No. 630479
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11441
- gi No. 630479
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11442
- gi No. 70636
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11443
- gi No. 70636
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11444
- gi No. 70637
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11445
- gi No. 70639
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11446
- gi No. 70639
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11447
- gi No. 70639
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11448
- gi No. 70640
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11449
- gi No. 70642
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11450
- gi No. 70642
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11451
- gi No. 70642
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11452
- gi No. 70642
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11453
- gi No. 70643
- % Identity 100
- Alignment Length 81
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11454
- gi No. 70644
- % Identity 100
- Alignment Length 99
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11455
- gi No. 70644
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11456
- gi No. 70644
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11457
- gi No. 70644
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11458
- gi No. 70644
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11459
- gi No. 70645
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11460
- gi No. 70645
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11461
- gi No. 70645
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11462
- gi No. 70645
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11463
- gi No. 70646
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11464
- gi No. 70647
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11465
- gi No. 70647
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11466

- gi No. 70648
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11467
- gi No. 70650
- % Identity 74.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11468
- gi No. 70653
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11469
- gi No. 70654
- % Identity 98.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11470
- gi No. 70657
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11471
- gi No. 70658
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11472
- gi No. 70659
- % Identity 96.9
- Alignment Length 65
- Location of Alignment in SEQ ID NO 1321: from 6 to 70

- Alignment No. 11473
- gi No. 70660
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11474
- gi No. 726391
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11475
- gi No. 726391
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11476
- gi No. 726391

- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11477
- gi No. 726391
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11478
- gi No. 726391
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11479
- gi No. 726391
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11480
- gi No. 726391
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11481
- gi No. 726391
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11482
- gi No. 726391
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11483
- gi No. 726391
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11484
- gi No. 82040
- % Identity 99.1
- Alignment Length 111
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11485
- gi No. 82040
- % Identity 100
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1321: from 1 to 36

- Alignment No. 11486
- gi No. 82040
- % Identity 100

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- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11487
- gi No. 82040
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11488
- gi No. 82284
- % Identity 100
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1321: from 1 to 56

- Alignment No. 11489
- gi No. 82286
- % Identity 100
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1321: from 57 to 70

- Alignment No. 11490
- gi No. 82287
- % Identity 100
- Alignment Length 48
- Location of Alignment in SEQ ID NO 1321: from 1 to 48

- Alignment No. 11491
- gi No. 82288
- % Identity 100
- Alignment Length 34
- Location of Alignment in SEQ ID NO 1321: from 37 to 70

- Alignment No. 11492
- gi No. 82426
- % Identity 100
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11493
- gi No. 82426
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11494
- gi No. 82512
- % Identity 100
- Alignment Length 106
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11495
- gi No. 82512
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11496
- gi No. 825728
- % Identity 96.8
- Alignment Length 31

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- Location of Alignment in SEQ ID NO 1321: from 40 to 70
- Alignment No. 11497
- gi No. 82733
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11498
- gi No. 82734
- % Identity 100
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11499
- gi No. 82734
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11500
- gi No. 82734
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11501
- gi No. 829173
- % Identity 93.1
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1321: from 13 to 70
- Alignment No. 11502
- gi No. 83594
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11503
- gi No. 83594
- % Identity 87.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1321: from 1 to 11
- Alignment No. 11504
- gi No. 83596
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11505
- gi No. 83596
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11506
- gi No. 83596
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11507
- gi No. 83596
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11508
- gi No. 84151
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11509
- gi No. 84151
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11510
- gi No. 84152
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11511
- gi No. 84152
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11512
- gi No. 84152
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11513
- gi No. 84152
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11514
- gi No. 84336
- % Identity 94.2
- Alignment Length 52
- Location of Alignment in SEQ ID NO 1321: from 19 to 70

- Alignment No. 11515
- gi No. 84337
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11516
- gi No. 84337
- % Identity 93.7
- Alignment Length 95
- Location of Alignment in SEQ ID NO 1321: from 1 to 19

- Alignment No. 11517
- gi No. 84478
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11518
- gi No. 84478
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11519
- gi No. 84478
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11520
- gi No. 84478
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11521
- gi No. 84478
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11522
- gi No. 84478
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11523
- gi No. 84478
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11524
- gi No. 84478
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11525
- gi No. 84478
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11526
- gi No. 84478
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11527

- gi No. 84834
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11528
- gi No. 84834
- % Identity 96.7
- Alignment Length 92
- Location of Alignment in SEQ ID NO 1321: from 1 to 16

- Alignment No. 11529
- gi No. 84834
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11530
- gi No. 85106
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11531
- gi No. 85106
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11532
- gi No. 86473
- % Identity 96.2
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1321: from 45 to 70

- Alignment No. 11533
- gi No. 870794
- % Identity 89.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11534
- gi No. 870794
- % Identity 75.5
- Alignment Length 149
- Location of Alignment in SEQ ID NO 1321: from 1 to 71

- Alignment No. 11535
- gi No. 870794
- % Identity 79.6
- Alignment Length 152
- Location of Alignment in SEQ ID NO 1321: from 1 to 69

- Alignment No. 11536
- gi No. 870794
- % Identity 70.5
- Alignment Length 167
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11537
- gi No. 89311

- % Identity 95.8
- Alignment Length 96
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11538
- gi No. 89311
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11539
- gi No. 89311
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11540
- gi No. 899115
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11541
- gi No. 899115
- % Identity 100
- Alignment Length 99
- Location of Alignment in SEQ ID NO 1321: from 1 to 23

- Alignment No. 11542
- gi No. 899608
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11543
- gi No. 899608
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11544
- gi No. 899608
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11545
- gi No. 899608
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11546
- gi No. 902525
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11547
- gi No. 902584
- % Identity 100

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- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11548
- gi No. 902584
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11549
- gi No. 902584
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11550
- gi No. 902584
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11551
- gi No. 902584
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11552
- gi No. 902584
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11553
- gi No. 902586
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11554
- gi No. 902586
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11555
- gi No. 902586
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11556
- gi No. 902586
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11557
- gi No. 91870
- % Identity 96
- Alignment Length 75

- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11558
- gi No. 91870
- % Identity 93.9
- Alignment Length 98
- Location of Alignment in SEQ ID NO 1321: from 1 to 22
- Alignment No. 11559
- gi No. 91871
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11560
- gi No. 9295
- % Identity 85.7
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1321: from 8 to 70
- Alignment No. 11561
- gi No. 940395
- % Identity 88.9
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1321: from 1 to 32
- Alignment No. 11562
- gi No. 940395
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11563
- gi No. 940395
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11564
- gi No. 940395
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11565
- gi No. 940395
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11566
- gi No. 940395
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11567
- gi No. 940395
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11568
- gi No. 940395
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11569
- gi No. 967985
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11570
- gi No. 99469
- % Identity 100
- Alignment Length 33
- Location of Alignment in SEQ ID NO 1321: from 38 to 70

- Alignment No. 11571
- gi No. 99771
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11572
- gi No. 99772
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11573
- gi No. 99975
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

Maximum Length Sequence corresponding to clone ID 254904

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1322
- Ceres seq_id 1500057

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1323
- Ceres seq_id 1500058
- Location of start within SEQ ID NO 1322: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11574
- Ezrin/radixin/moesin family
- Location within SEQ ID NO 1323: from 144 to 304 aa.

- Alignment No. 11575
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 1323: from 129 to 346 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1324
- Ceres seq_id 1500059

- Location of start within SEQ ID NO 1322: at 118 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11576
- Ezrin/radixin/moesin family
- Location within SEQ ID NO 1324: from 105 to 265 aa.
- Alignment No. 11577
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 1324: from 90 to 307 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1325
- Ceres seq_id 1500060
- Location of start within SEQ ID NO 1322: at 142 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11578
- Ezrin/radixin/moesin family
- Location within SEQ ID NO 1325: from 97 to 257 aa.
- Alignment No. 11579
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 1325: from 82 to 299 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 255048

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1326
- Ceres seq_id 1500065

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1327
- Ceres seq_id 1500066
- Location of start within SEQ ID NO 1326: at 199 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 11580
- gi No. 1041702
- % Identity 86.6
- Alignment Length 236
- Location of Alignment in SEQ ID NO 1327: from 19 to 118
- Alignment No. 11581
- gi No. 1778097
- % Identity 71.4
- Alignment Length 84
- Location of Alignment in SEQ ID NO 1327: from 4 to 87
- Alignment No. 11582
- gi No. 1778107
- % Identity 72.6
- Alignment Length 84
- Location of Alignment in SEQ ID NO 1327: from 1 to 82

- Alignment No. 11583
- gi No. 1778109
- % Identity 71.3
- Alignment Length 80
- Location of Alignment in SEQ ID NO 1327: from 1 to 77

- Alignment No. 11584
- gi No. 3461833
- % Identity 73.8
- Alignment Length 241
- Location of Alignment in SEQ ID NO 1327: from 14 to 118

- Alignment No. 11585
- gi No. 4027897
- % Identity 70.2
- Alignment Length 249
- Location of Alignment in SEQ ID NO 1327: from 1 to 118

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1328
- Ceres seq_id 1500067
- Location of start within SEQ ID NO 1326: at 241 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 11586
- gi No. 1041702
- % Identity 86.6
- Alignment Length 236
- Location of Alignment in SEQ ID NO 1328: from 5 to 104

- Alignment No. 11587
- gi No. 1778097
- % Identity 71.4
- Alignment Length 84
- Location of Alignment in SEQ ID NO 1328: from 1 to 73

- Alignment No. 11588
- gi No. 1778107
- % Identity 72.6
- Alignment Length 84
- Location of Alignment in SEQ ID NO 1328: from 1 to 68

- Alignment No. 11589
- gi No. 1778109
- % Identity 71.3
- Alignment Length 80
- Location of Alignment in SEQ ID NO 1328: from 1 to 63

- Alignment No. 11590
- gi No. 3461833
- % Identity 73.8
- Alignment Length 241
- Location of Alignment in SEQ ID NO 1328: from 1 to 104

- Alignment No. 11591
- gi No. 4027897
- % Identity 70.2
- Alignment Length 249
- Location of Alignment in SEQ ID NO 1328: from 1 to 104

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1329
- Ceres seq_id 1500068
- Location of start within SEQ ID NO 1326: at 740 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 255050

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1330
- Ceres seq_id 1500069

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1331
- Ceres seq_id 1500070
- Location of start within SEQ ID NO 1330: at 200 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11592
- TBC domain
- Location within SEQ ID NO 1331: from 113 to 327 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1332
- Ceres seq_id 1500071
- Location of start within SEQ ID NO 1330: at 233 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11593
- TBC domain
- Location within SEQ ID NO 1332: from 102 to 316 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1333
- Ceres seq_id 1500072
- Location of start within SEQ ID NO 1330: at 659 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11594
- TBC domain
- Location within SEQ ID NO 1333: from 1 to 174 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 255298

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1334
- Ceres seq_id 1500073

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1335
- Ceres seq_id 1500074
- Location of start within SEQ ID NO 1334: at 363 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11595
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1335: from 78 to 348 aa.

(D) Related Amino Acid Sequences

- Alignment No. 11596
- gi No. 1778440
- % Identity 72.3
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1335: from 215 to 261
- Alignment No. 11597
- gi No. 1778442
- % Identity 71.6
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1335: from 189 to 262
- Alignment No. 11598
- gi No. 1778444
- % Identity 78.4
- Alignment Length 51
- Location of Alignment in SEQ ID NO 1335: from 200 to 250

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1336
- Ceres seq_id 1500075
- Location of start within SEQ ID NO 1334: at 735 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11599
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1336: from 1 to 224 aa.

(D) Related Amino Acid Sequences

- Alignment No. 11600
- gi No. 1778440
- % Identity 72.3
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1336: from 91 to 137
- Alignment No. 11601
- gi No. 1778442
- % Identity 71.6
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1336: from 65 to 138
- Alignment No. 11602
- gi No. 1778444
- % Identity 78.4
- Alignment Length 51
- Location of Alignment in SEQ ID NO 1336: from 76 to 126

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1337
- Ceres seq_id 1500076
- Location of start within SEQ ID NO 1334: at 822 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11603
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1337: from 1 to 195 aa.

(D) Related Amino Acid Sequences

- Alignment No. 11604
- gi No. 1778440
- % Identity 72.3
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1337: from 62 to 108
- Alignment No. 11605
- gi No. 1778442
- % Identity 71.6
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1337: from 36 to 109
- Alignment No. 11606
- gi No. 1778444
- % Identity 78.4
- Alignment Length 51
- Location of Alignment in SEQ ID NO 1337: from 47 to 97

Maximum Length Sequence corresponding to clone ID 255307

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1338
- Ceres seq_id 1500077

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1339
- Ceres seq_id 1500078
- Location of start within SEQ ID NO 1338: at 90 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11607
- Polygalacturonase (pectinase)
- Location within SEQ ID NO 1339: from 97 to 436 aa.

(D) Related Amino Acid Sequences

- Alignment No. 11608
- gi No. 1346702
- % Identity 100
- Alignment Length 444
- Location of Alignment in SEQ ID NO 1339: from 1 to 444
- Alignment No. 11609
- gi No. 3004442
- % Identity 97.5
- Alignment Length 445
- Location of Alignment in SEQ ID NO 1339: from 1 to 444
- Alignment No. 11610
- gi No. 421833
- % Identity 97.3
- Alignment Length 445
- Location of Alignment in SEQ ID NO 1339: from 1 to 444

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1340

- Ceres seq_id 1500079
- Location of start within SEQ ID NO 1338: at 141 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11611
- Polygalacturonase (pectinase)
- Location within SEQ ID NO 1340: from 80 to 419 aa.

(D) Related Amino Acid Sequences

- Alignment No. 11612
- gi No. 1346702
- % Identity 100
- Alignment Length 444
- Location of Alignment in SEQ ID NO 1340: from 1 to 427

- Alignment No. 11613
- gi No. 3004442
- % Identity 97.5
- Alignment Length 445
- Location of Alignment in SEQ ID NO 1340: from 1 to 427

- Alignment No. 11614
- gi No. 421833
- % Identity 97.3
- Alignment Length 445
- Location of Alignment in SEQ ID NO 1340: from 1 to 427

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1341
- Ceres seq_id 1500080
- Location of start within SEQ ID NO 1338: at 420 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11615
- Polygalacturonase (pectinase)
- Location within SEQ ID NO 1341: from 1 to 326 aa.

(D) Related Amino Acid Sequences

- Alignment No. 11616
- gi No. 1346702
- % Identity 100
- Alignment Length 444
- Location of Alignment in SEQ ID NO 1341: from 1 to 334

- Alignment No. 11617
- gi No. 3004442
- % Identity 97.5
- Alignment Length 445
- Location of Alignment in SEQ ID NO 1341: from 1 to 334

- Alignment No. 11618
- gi No. 421833
- % Identity 97.3
- Alignment Length 445
- Location of Alignment in SEQ ID NO 1341: from 1 to 334

Maximum Length Sequence corresponding to clone ID 255364

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1342

- Ceres seq_id 1500081

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1343
- Ceres seq_id 1500082
- Location of start within SEQ ID NO 1342: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 11619
- gi No. 4768976
- % Identity 71.7
- Alignment Length 92
- Location of Alignment in SEQ ID NO 1343: from 246 to 337

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1344
- Ceres seq_id 1500083
- Location of start within SEQ ID NO 1342: at 94 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 11620
- gi No. 4768976
- % Identity 71.7
- Alignment Length 92
- Location of Alignment in SEQ ID NO 1344: from 215 to 306

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1345
- Ceres seq_id 1500084
- Location of start within SEQ ID NO 1342: at 277 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 11621
- gi No. 4768976
- % Identity 71.7
- Alignment Length 92
- Location of Alignment in SEQ ID NO 1345: from 154 to 245

Maximum Length Sequence corresponding to clone ID 255477

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1346
- Ceres seq_id 1500085

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1347
- Ceres seq_id 1500086
- Location of start within SEQ ID NO 1346: at 286 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 11622
- gi No. 5430753
- % Identity 81.9
- Alignment Length 234
- Location of Alignment in SEQ ID NO 1347: from 110 to 341

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1348
- Ceres seq_id 1500087
- Location of start within SEQ ID NO 1346: at 613 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 11623
- gi No. 5430753
- % Identity 81.9
- Alignment Length 234
- Location of Alignment in SEQ ID NO 1348: from 1 to 232

Maximum Length Sequence corresponding to clone ID 255542

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1349
- Ceres seq_id 1500088

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1350
- Ceres seq_id 1500089
- Location of start within SEQ ID NO 1349: at 51 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 11624
- gi No. 100214
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1350: from 329 to 346
- Alignment No. 11625
- gi No. 100214
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1350: from 329 to 346
- Alignment No. 11626
- gi No. 100216
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1350: from 329 to 346
- Alignment No. 11627
- gi No. 102424
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1350: from 279 to 293
- Alignment No. 11628
- gi No. 102427
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293
- Alignment No. 11629
- gi No. 1061334
- % Identity 82.4
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1350: from 279 to 295

- Alignment No. 11630
- gi No. 1065941
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1350: from 282 to 294

- Alignment No. 11631
- gi No. 1065941
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 1350: from 280 to 293

- Alignment No. 11632
- gi No. 1065941
- % Identity 72.2
- Alignment Length 19
- Location of Alignment in SEQ ID NO 1350: from 329 to 345

- Alignment No. 11633
- gi No. 1076555
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1350: from 329 to 346

- Alignment No. 11634
- gi No. 108231
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293

- Alignment No. 11635
- gi No. 113210
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293

- Alignment No. 11636
- gi No. 1163054
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293

- Alignment No. 11637
- gi No. 1163054
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 1350: from 280 to 293

- Alignment No. 11638
- gi No. 1185397
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1350: from 329 to 339

- Alignment No. 11639
- gi No. 1185397
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1350: from 280 to 293

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- Alignment No. 11640
- gi No. 1185397
- % Identity 81.3
- Alignment Length 16
- Location of Alignment in SEQ ID NO 1350: from 280 to 294
- Alignment No. 11641
- gi No. 119111
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293
- Alignment No. 11642
- gi No. 119111
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293
- Alignment No. 11643
- gi No. 1326381
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1350: from 323 to 337
- Alignment No. 11644
- gi No. 1345537
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1350: from 329 to 346
- Alignment No. 11645
- gi No. 134920
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1350: from 329 to 339
- Alignment No. 11646
- gi No. 134920
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1350: from 329 to 348
- Alignment No. 11647
- gi No. 1351865
- % Identity 84.6
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1350: from 281 to 293
- Alignment No. 11648
- gi No. 141279
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293
- Alignment No. 11649
- gi No. 141279
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293
- Alignment No. 11650

- gi No. 141279
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293

- Alignment No. 11651
- gi No. 141279
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293

- Alignment No. 11652
- gi No. 141279
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293

- Alignment No. 11653
- gi No. 141279
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293

- Alignment No. 11654
- gi No. 141279
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293

- Alignment No. 11655
- gi No. 141279
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293

- Alignment No. 11656
- gi No. 141279
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293

- Alignment No. 11657
- gi No. 1480413
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293

- Alignment No. 11658
- gi No. 1644457
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1350: from 329 to 339

- Alignment No. 11659
- gi No. 1644459
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1350: from 329 to 339

- Alignment No. 11660
- gi No. 1644461

- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1350: from 329 to 339

- Alignment No. 11661
- gi No. 1655699
- % Identity 100
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1350: from 329 to 339

- Alignment No. 11662
- gi No. 1655699
- % Identity 92.9
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293

- Alignment No. 11663
- gi No. 1655699
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1350: from 329 to 346

- Alignment No. 11664
- gi No. 1655699
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1350: from 329 to 346

- Alignment No. 11665
- gi No. 169345
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1350: from 329 to 346

- Alignment No. 11666
- gi No. 1911629
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293

- Alignment No. 11667
- gi No. 1911629
- % Identity 86.7
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1350: from 280 to 294

- Alignment No. 11668
- gi No. 1914851
- % Identity 92.9
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293

- Alignment No. 11669
- gi No. 1914851
- % Identity 82.4
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1350: from 278 to 293

- Alignment No. 11670
- gi No. 1914851
- % Identity 77.8

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- Alignment Length 18
- Location of Alignment in SEQ ID NO 1350: from 278 to 293
- Alignment No. 11671
- gi No. 1914851
- % Identity 73.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 1350: from 278 to 293
- Alignment No. 11672
- gi No. 2108256
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1350: from 329 to 346
- Alignment No. 11673
- gi No. 2108256
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1350: from 329 to 346
- Alignment No. 11674
- gi No. 2129478
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1350: from 280 to 293
- Alignment No. 11675
- gi No. 2147342
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 323 to 336
- Alignment No. 11676
- gi No. 2147342
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 1350: from 323 to 338
- Alignment No. 11677
- gi No. 226743
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1350: from 329 to 348
- Alignment No. 11678
- gi No. 2494630
- % Identity 90.9
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1350: from 283 to 293
- Alignment No. 11679
- gi No. 2494630
- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1350: from 329 to 340
- Alignment No. 11680
- gi No. 3204132
- % Identity 77.8
- Alignment Length 18

- Location of Alignment in SEQ ID NO 1350: from 329 to 346
- Alignment No. 11681
- gi No. 3204132
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1350: from 327 to 346
- Alignment No. 11682
- gi No. 322758
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293
- Alignment No. 11683
- gi No. 322758
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1350: from 280 to 291
- Alignment No. 11684
- gi No. 347455
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1350: from 327 to 346
- Alignment No. 11685
- gi No. 3875441
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1350: from 324 to 334
- Alignment No. 11686
- gi No. 3875441
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1350: from 324 to 334
- Alignment No. 11687
- gi No. 4008584
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1350: from 329 to 340
- Alignment No. 11688
- gi No. 4033606
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1350: from 329 to 346
- Alignment No. 11689
- gi No. 4096360
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1350: from 329 to 339
- Alignment No. 11690
- gi No. 4096360
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1350: from 280 to 293

- Alignment No. 11691
- gi No. 4096360
- % Identity 81.3
- Alignment Length 16
- Location of Alignment in SEQ ID NO 1350: from 280 to 294

- Alignment No. 11692
- gi No. 4467884
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1350: from 329 to 346

- Alignment No. 11693
- gi No. 4522026
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1350: from 329 to 347

- Alignment No. 11694
- gi No. 4589678
- % Identity 91.7
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1350: from 329 to 340

- Alignment No. 11695
- gi No. 497413
- % Identity 90.9
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1350: from 283 to 293

- Alignment No. 11696
- gi No. 497413
- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1350: from 329 to 340

- Alignment No. 11697
- gi No. 5302801
- % Identity 99.6
- Alignment Length 473
- Location of Alignment in SEQ ID NO 1350: from 1 to 473

- Alignment No. 11698
- gi No. 5441495
- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1350: from 329 to 340

- Alignment No. 11699
- gi No. 5441495
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1350: from 331 to 343

- Alignment No. 11700
- gi No. 628112
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293

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- Alignment No. 11701
- gi No. 628112
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293

- Alignment No. 11702
- gi No. 628185
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293

- Alignment No. 11703
- gi No. 628185
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293

- Alignment No. 11704
- gi No. 628185
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293

- Alignment No. 11705
- gi No. 628185
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293

- Alignment No. 11706
- gi No. 628185
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1350: from 280 to 294

- Alignment No. 11707
- gi No. 81870
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1350: from 329 to 346

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1351
- Ceres seq_id 1500090
- Location of start within SEQ ID NO 1349: at 492 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 11708
- gi No. 100214
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1351: from 182 to 199

- Alignment No. 11709
- gi No. 100214
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1351: from 182 to 199

- Alignment No. 11710
- gi No. 100216
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1351: from 182 to 199

- Alignment No. 11711
- gi No. 102424
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1351: from 132 to 146

- Alignment No. 11712
- gi No. 102427
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146

- Alignment No. 11713
- gi No. 1061334
- % Identity 82.4
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1351: from 132 to 148

- Alignment No. 11714
- gi No. 1065941
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1351: from 135 to 147

- Alignment No. 11715
- gi No. 1065941
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 1351: from 133 to 146

- Alignment No. 11716
- gi No. 1065941
- % Identity 72.2
- Alignment Length 19
- Location of Alignment in SEQ ID NO 1351: from 182 to 198

- Alignment No. 11717
- gi No. 1076555
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1351: from 182 to 199

- Alignment No. 11718
- gi No. 108231
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146

- Alignment No. 11719
- gi No. 113210
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146

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- Alignment No. 11720
- gi No. 1163054
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146

- Alignment No. 11721
- gi No. 1163054
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 1351: from 133 to 146

- Alignment No. 11722
- gi No. 1185397
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1351: from 182 to 192

- Alignment No. 11723
- gi No. 1185397
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1351: from 133 to 146

- Alignment No. 11724
- gi No. 1185397
- % Identity 81.3
- Alignment Length 16
- Location of Alignment in SEQ ID NO 1351: from 133 to 147

- Alignment No. 11725
- gi No. 119111
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146

- Alignment No. 11726
- gi No. 119111
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146

- Alignment No. 11727
- gi No. 1326381
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1351: from 176 to 190

- Alignment No. 11728
- gi No. 1345537
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1351: from 182 to 199

- Alignment No. 11729
- gi No. 134920
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1351: from 182 to 192

- Alignment No. 11730

- gi No. 134920
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1351: from 182 to 201

- Alignment No. 11731
- gi No. 1351865
- % Identity 84.6
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1351: from 134 to 146

- Alignment No. 11732
- gi No. 141279
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146

- Alignment No. 11733
- gi No. 141279
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146

- Alignment No. 11734
- gi No. 141279
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146

- Alignment No. 11735
- gi No. 141279
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146

- Alignment No. 11736
- gi No. 141279
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146

- Alignment No. 11737
- gi No. 141279
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146

- Alignment No. 11738
- gi No. 141279
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146

- Alignment No. 11739
- gi No. 141279
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146

- Alignment No. 11740
- gi No. 141279

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- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146

- Alignment No. 11741
- gi No. 1480413
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146

- Alignment No. 11742
- gi No. 1644457
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1351: from 182 to 192

- Alignment No. 11743
- gi No. 1644459
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1351: from 182 to 192

- Alignment No. 11744
- gi No. 1644461
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1351: from 182 to 192

- Alignment No. 11745
- gi No. 1655699
- % Identity 100
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1351: from 182 to 192

- Alignment No. 11746
- gi No. 1655699
- % Identity 92.9
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146

- Alignment No. 11747
- gi No. 1655699
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1351: from 182 to 199

- Alignment No. 11748
- gi No. 1655699
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1351: from 182 to 199

- Alignment No. 11749
- gi No. 169345
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1351: from 182 to 199

- Alignment No. 11750
- gi No. 1911629
- % Identity 78.6

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- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146

- Alignment No. 11751
- gi No. 1911629
- % Identity 86.7
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1351: from 133 to 147

- Alignment No. 11752
- gi No. 1914851
- % Identity 92.9
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146

- Alignment No. 11753
- gi No. 1914851
- % Identity 82.4
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1351: from 131 to 146

- Alignment No. 11754
- gi No. 1914851
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1351: from 131 to 146

- Alignment No. 11755
- gi No. 1914851
- % Identity 73.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 1351: from 131 to 146

- Alignment No. 11756
- gi No. 2108256
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1351: from 182 to 199

- Alignment No. 11757
- gi No. 2108256
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1351: from 182 to 199

- Alignment No. 11758
- gi No. 2129478
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1351: from 133 to 146

- Alignment No. 11759
- gi No. 2147342
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 176 to 189

- Alignment No. 11760
- gi No. 2147342
- % Identity 75
- Alignment Length 16

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- Location of Alignment in SEQ ID NO 1351: from 176 to 191
- Alignment No. 11761
- gi No. 226743
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1351: from 182 to 201
- Alignment No. 11762
- gi No. 2494630
- % Identity 90.9
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1351: from 136 to 146
- Alignment No. 11763
- gi No. 2494630
- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1351: from 182 to 193
- Alignment No. 11764
- gi No. 3204132
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1351: from 182 to 199
- Alignment No. 11765
- gi No. 3204132
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1351: from 180 to 199
- Alignment No. 11766
- gi No. 322758
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146
- Alignment No. 11767
- gi No. 322758
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1351: from 133 to 144
- Alignment No. 11768
- gi No. 347455
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1351: from 180 to 199
- Alignment No. 11769
- gi No. 3875441
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1351: from 177 to 187
- Alignment No. 11770
- gi No. 3875441
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1351: from 177 to 187

- Alignment No. 11771
- gi No. 4008584
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1351: from 182 to 193

- Alignment No. 11772
- gi No. 4033606
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1351: from 182 to 199

- Alignment No. 11773
- gi No. 4096360
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1351: from 182 to 192

- Alignment No. 11774
- gi No. 4096360
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1351: from 133 to 146

- Alignment No. 11775
- gi No. 4096360
- % Identity 81.3
- Alignment Length 16
- Location of Alignment in SEQ ID NO 1351: from 133 to 147

- Alignment No. 11776
- gi No. 4467884
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1351: from 182 to 199

- Alignment No. 11777
- gi No. 4522026
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1351: from 182 to 200

- Alignment No. 11778
- gi No. 4589678
- % Identity 91.7
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1351: from 182 to 193

- Alignment No. 11779
- gi No. 497413
- % Identity 90.9
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1351: from 136 to 146

- Alignment No. 11780
- gi No. 497413
- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1351: from 182 to 193

- Alignment No. 11781
- gi No. 5302801
- % Identity 99.6
- Alignment Length 473
- Location of Alignment in SEQ ID NO 1351: from 1 to 326

- Alignment No. 11782
- gi No. 5441495
- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1351: from 182 to 193

- Alignment No. 11783
- gi No. 5441495
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1351: from 184 to 196

- Alignment No. 11784
- gi No. 628112
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146

- Alignment No. 11785
- gi No. 628112
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146

- Alignment No. 11786
- gi No. 628185
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146

- Alignment No. 11787
- gi No. 628185
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146

- Alignment No. 11788
- gi No. 628185
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146

- Alignment No. 11789
- gi No. 628185
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146

- Alignment No. 11790
- gi No. 628185
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1351: from 133 to 147

- Alignment No. 11791

- gi No. 81870
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1351: from 182 to 199

Maximum Length Sequence corresponding to clone ID 255685

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1352
- Ceres seq_id 1500091

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1353
- Ceres seq_id 1500092
- Location of start within SEQ ID NO 1352: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11792
- Lipase/Acylhydrolase with GDSL-like motif
- Location within SEQ ID NO 1353: from 1 to 80 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1354
- Ceres seq_id 1500093
- Location of start within SEQ ID NO 1352: at 434 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 255876

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1355
- Ceres seq_id 1500097

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1356
- Ceres seq_id 1500098
- Location of start within SEQ ID NO 1355: at 52 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11793
- Lyase
- Location within SEQ ID NO 1356: from 63 to 473 aa.

(D) Related Amino Acid Sequences

- Alignment No. 11794
- gi No. 2252472
- % Identity 100
- Alignment Length 474
- Location of Alignment in SEQ ID NO 1356: from 1 to 473

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1357
- Ceres seq_id 1500099
- Location of start within SEQ ID NO 1355: at 190 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11795

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- Lyase
- Location within SEQ ID NO 1357: from 17 to 427 aa.

(D) Related Amino Acid Sequences

- Alignment No. 11796
- gi No. 2252472
- % Identity 100
- Alignment Length 474
- Location of Alignment in SEQ ID NO 1357: from 1 to 427

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1358
- Ceres seq_id 1500100
- Location of start within SEQ ID NO 1355: at 325 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11797
- Lyase
- Location within SEQ ID NO 1358: from 1 to 382 aa.

(D) Related Amino Acid Sequences

- Alignment No. 11798
- gi No. 2252472
- % Identity 100
- Alignment Length 474
- Location of Alignment in SEQ ID NO 1358: from 1 to 382

Maximum Length Sequence corresponding to clone ID 256052

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1359
- Ceres seq_id 1500101

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1360
- Ceres seq_id 1500102
- Location of start within SEQ ID NO 1359: at 129 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11799
- NifU-like domain
- Location within SEQ ID NO 1360: from 89 to 155 aa.
- Alignment No. 11800
- NifU-like domain
- Location within SEQ ID NO 1360: from 171 to 233 aa.

(D) Related Amino Acid Sequences

- Alignment No. 11801
- gi No. 4538920
- % Identity 99.1
- Alignment Length 224
- Location of Alignment in SEQ ID NO 1360: from 13 to 236

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1361
- Ceres seq_id 1500103
- Location of start within SEQ ID NO 1359: at 165 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11802
- NifU-like domain
- Location within SEQ ID NO 1361: from 77 to 143 aa.
- Alignment No. 11803
- NifU-like domain
- Location within SEQ ID NO 1361: from 159 to 221 aa.

(D) Related Amino Acid Sequences

- Alignment No. 11804
- gi No. 4538920
- % Identity 99.1
- Alignment Length 224
- Location of Alignment in SEQ ID NO 1361: from 1 to 224

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1362
- Ceres seq_id 1500104
- Location of start within SEQ ID NO 1359: at 372 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11805
- NifU-like domain
- Location within SEQ ID NO 1362: from 8 to 74 aa.
- Alignment No. 11806
- NifU-like domain
- Location within SEQ ID NO 1362: from 90 to 152 aa.

(D) Related Amino Acid Sequences

- Alignment No. 11807
- gi No. 4538920
- % Identity 99.1
- Alignment Length 224
- Location of Alignment in SEQ ID NO 1362: from 1 to 155

Maximum Length Sequence corresponding to clone ID 256076

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1363
- Ceres seq_id 1500105

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1364
- Ceres seq_id 1500106
- Location of start within SEQ ID NO 1363: at 424 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11808
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1364: from 1 to 240 aa.

(D) Related Amino Acid Sequences

- Alignment No. 11809
- gi No. 1076387
- % Identity 76.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245
- Alignment No. 11810
- gi No. 1076641

- % Identity 82.8
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245

- Alignment No. 11811
- gi No. 1076649
- % Identity 82.8
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245

- Alignment No. 11812
- gi No. 1076651
- % Identity 79.6
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245

- Alignment No. 11813
- gi No. 1170711
- % Identity 82.5
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245

- Alignment No. 11814
- gi No. 1170714
- % Identity 83.5
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245

- Alignment No. 11815
- gi No. 125373
- % Identity 70.8
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 244

- Alignment No. 11816
- gi No. 125374
- % Identity 70.9
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1364: from 1 to 245

- Alignment No. 11817
- gi No. 1431622
- % Identity 82.5
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245

- Alignment No. 11818
- gi No. 1480078
- % Identity 91.2
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245

- Alignment No. 11819
- gi No. 1504063
- % Identity 76.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245

- Alignment No. 11820
- gi No. 1617200
- % Identity 81.1

- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245

- Alignment No. 11821
- gi No. 1709127
- % Identity 82.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245

- Alignment No. 11822
- gi No. 1709128
- % Identity 81.7
- Alignment Length 284
- Location of Alignment in SEQ ID NO 1364: from 1 to 245

- Alignment No. 11823
- gi No. 1709129
- % Identity 82.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245

- Alignment No. 11824
- gi No. 1730039
- % Identity 70.8
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 244

- Alignment No. 11825
- gi No. 1877393
- % Identity 83
- Alignment Length 171
- Location of Alignment in SEQ ID NO 1364: from 76 to 245

- Alignment No. 11826
- gi No. 1877397
- % Identity 93.4
- Alignment Length 226
- Location of Alignment in SEQ ID NO 1364: from 20 to 245

- Alignment No. 11827
- gi No. 1944518
- % Identity 79
- Alignment Length 290
- Location of Alignment in SEQ ID NO 1364: from 1 to 250

- Alignment No. 11828
- gi No. 2117783
- % Identity 70.9
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1364: from 1 to 245

- Alignment No. 11829
- gi No. 2117784
- % Identity 70.2
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1364: from 1 to 245

- Alignment No. 11830
- gi No. 2129738
- % Identity 90.5
- Alignment Length 285

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- Location of Alignment in SEQ ID NO 1364: from 1 to 245
- Alignment No. 11831
- gi No. 2129739
- % Identity 96.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245
- Alignment No. 11832
- gi No. 2160191
- % Identity 76.5
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245
- Alignment No. 11833
- gi No. 2182029
- % Identity 89.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245
- Alignment No. 11834
- gi No. 2191169
- % Identity 78.7
- Alignment Length 300
- Location of Alignment in SEQ ID NO 1364: from 1 to 245
- Alignment No. 11835
- gi No. 2398519
- % Identity 82.5
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245
- Alignment No. 11836
- gi No. 2569931
- % Identity 74.1
- Alignment Length 290
- Location of Alignment in SEQ ID NO 1364: from 1 to 250
- Alignment No. 11837
- gi No. 2569950
- % Identity 79.9
- Alignment Length 284
- Location of Alignment in SEQ ID NO 1364: from 1 to 244
- Alignment No. 11838
- gi No. 2598601
- % Identity 77.9
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245
- Alignment No. 11839
- gi No. 2598603
- % Identity 78.6
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245
- Alignment No. 11840
- gi No. 2641994
- % Identity 70.8
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 244

- Alignment No. 11841
- gi No. 2911533
- % Identity 79.6
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245

- Alignment No. 11842
- gi No. 3201623
- % Identity 91.2
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245

- Alignment No. 11843
- gi No. 3236115
- % Identity 81.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245

- Alignment No. 11844
- gi No. 3236117
- % Identity 80
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245

- Alignment No. 11845
- gi No. 3250738
- % Identity 73.7
- Alignment Length 293
- Location of Alignment in SEQ ID NO 1364: from 1 to 250

- Alignment No. 11846
- gi No. 3264607
- % Identity 81.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1364: from 176 to 245

- Alignment No. 11847
- gi No. 3702608
- % Identity 77.2
- Alignment Length 290
- Location of Alignment in SEQ ID NO 1364: from 1 to 250

- Alignment No. 11848
- gi No. 3928148
- % Identity 81.6
- Alignment Length 266
- Location of Alignment in SEQ ID NO 1364: from 1 to 245

- Alignment No. 11849
- gi No. 402652
- % Identity 70.9
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1364: from 1 to 245

- Alignment No. 11850
- gi No. 4140287
- % Identity 71.6
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1364: from 1 to 245

- ```
- Alignment No. 11855
- gi No. 1076387
- % Identity 76.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242

- Alignment No. 11856
- gi No. 1076641
- % Identity 82.8
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242

- Alignment No. 11857
- gi No. 1076649
- % Identity 82.8
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242

- Alignment No. 11858
- gi No. 1076651
- % Identity 79.6
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242

- Alignment No. 11859
- gi No. 1170711
- % Identity 82.5
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242

- Alignment No. 11860
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- gi No. 1170714
- % Identity 83.5
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
  
- Alignment No. 11861
- gi No. 125373
- % Identity 70.8
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 241
  
- Alignment No. 11862
- gi No. 125374
- % Identity 70.9
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
  
- Alignment No. 11863
- gi No. 1431622
- % Identity 82.5
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
  
- Alignment No. 11864
- gi No. 1480078
- % Identity 91.2
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
  
- Alignment No. 11865
- gi No. 1504063
- % Identity 76.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
  
- Alignment No. 11866
- gi No. 1617200
- % Identity 81.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
  
- Alignment No. 11867
- gi No. 1709127
- % Identity 82.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
  
- Alignment No. 11868
- gi No. 1709128
- % Identity 81.7
- Alignment Length 284
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
  
- Alignment No. 11869
- gi No. 1709129
- % Identity 82.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
  
- Alignment No. 11870
- gi No. 1730039

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- % Identity 70.8
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 241
  
- Alignment No. 11871
- gi No. 1877393
- % Identity 83
- Alignment Length 171
- Location of Alignment in SEQ ID NO 1365: from 73 to 242
  
- Alignment No. 11872
- gi No. 1877397
- % Identity 93.4
- Alignment Length 226
- Location of Alignment in SEQ ID NO 1365: from 17 to 242
  
- Alignment No. 11873
- gi No. 1944518
- % Identity 79
- Alignment Length 290
- Location of Alignment in SEQ ID NO 1365: from 1 to 247
  
- Alignment No. 11874
- gi No. 2117783
- % Identity 70.9
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
  
- Alignment No. 11875
- gi No. 2117784
- % Identity 70.2
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
  
- Alignment No. 11876
- gi No. 2129738
- % Identity 90.5
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
  
- Alignment No. 11877
- gi No. 2129739
- % Identity 96.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
  
- Alignment No. 11878
- gi No. 2160191
- % Identity 76.5
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
  
- Alignment No. 11879
- gi No. 2182029
- % Identity 89.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
  
- Alignment No. 11880
- gi No. 2191169
- % Identity 78.7

- Alignment Length 300
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
  
- Alignment No. 11881
- gi No. 2398519
- % Identity 82.5
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
  
- Alignment No. 11882
- gi No. 2569931
- % Identity 74.1
- Alignment Length 290
- Location of Alignment in SEQ ID NO 1365: from 1 to 247
  
- Alignment No. 11883
- gi No. 2569950
- % Identity 79.9
- Alignment Length 284
- Location of Alignment in SEQ ID NO 1365: from 1 to 241
  
- Alignment No. 11884
- gi No. 2598601
- % Identity 77.9
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
  
- Alignment No. 11885
- gi No. 2598603
- % Identity 78.6
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
  
- Alignment No. 11886
- gi No. 2641994
- % Identity 70.8
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 241
  
- Alignment No. 11887
- gi No. 2911533
- % Identity 79.6
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
  
- Alignment No. 11888
- gi No. 3201623
- % Identity 91.2
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
  
- Alignment No. 11889
- gi No. 3236115
- % Identity 81.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
  
- Alignment No. 11890
- gi No. 3236117
- % Identity 80
- Alignment Length 285

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- Location of Alignment in SEQ ID NO 1365: from 1 to 242
- Alignment No. 11891
- gi No. 3250738
- % Identity 73.7
- Alignment Length 293
- Location of Alignment in SEQ ID NO 1365: from 1 to 247
- Alignment No. 11892
- gi No. 3264607
- % Identity 81.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1365: from 173 to 242
- Alignment No. 11893
- gi No. 3702608
- % Identity 77.2
- Alignment Length 290
- Location of Alignment in SEQ ID NO 1365: from 1 to 247
- Alignment No. 11894
- gi No. 3928148
- % Identity 81.6
- Alignment Length 266
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
- Alignment No. 11895
- gi No. 402652
- % Identity 70.9
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
- Alignment No. 11896
- gi No. 4140287
- % Identity 71.6
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
- Alignment No. 11897
- gi No. 4504163
- % Identity 70.9
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
- Alignment No. 11898
- gi No. 4539390
- % Identity 100
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
- Alignment No. 11899
- gi No. 5070700
- % Identity 70.9
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1365: from 1 to 242

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1366
- Ceres seq\_id 1500108
- Location of start within SEQ ID NO 1363: at 514 nt.

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(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11900
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1366: from 1 to 210 aa.

(D) Related Amino Acid Sequences

- Alignment No. 11901
- gi No. 1076387
- % Identity 76.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
- Alignment No. 11902
- gi No. 1076641
- % Identity 82.8
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
- Alignment No. 11903
- gi No. 1076649
- % Identity 82.8
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
- Alignment No. 11904
- gi No. 1076651
- % Identity 79.6
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
- Alignment No. 11905
- gi No. 1170711
- % Identity 82.5
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
- Alignment No. 11906
- gi No. 1170714
- % Identity 83.5
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
- Alignment No. 11907
- gi No. 125373
- % Identity 70.8
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 214
- Alignment No. 11908
- gi No. 125374
- % Identity 70.9
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
- Alignment No. 11909
- gi No. 1431622
- % Identity 82.5
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215

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- Alignment No. 11910
- gi No. 1480078
- % Identity 91.2
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
- Alignment No. 11911
- gi No. 1504063
- % Identity 76.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
- Alignment No. 11912
- gi No. 1617200
- % Identity 81.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
- Alignment No. 11913
- gi No. 1709127
- % Identity 82.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
- Alignment No. 11914
- gi No. 1709128
- % Identity 81.7
- Alignment Length 284
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
- Alignment No. 11915
- gi No. 1709129
- % Identity 82.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
- Alignment No. 11916
- gi No. 1730039
- % Identity 70.8
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 214
- Alignment No. 11917
- gi No. 1877393
- % Identity 83
- Alignment Length 171
- Location of Alignment in SEQ ID NO 1366: from 46 to 215
- Alignment No. 11918
- gi No. 1877397
- % Identity 93.4
- Alignment Length 226
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
- Alignment No. 11919
- gi No. 1944518
- % Identity 79
- Alignment Length 290
- Location of Alignment in SEQ ID NO 1366: from 1 to 220
- Alignment No. 11920

- gi No. 2117783
- % Identity 70.9
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
  
- Alignment No. 11921
- gi No. 2117784
- % Identity 70.2
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
  
- Alignment No. 11922
- gi No. 2129738
- % Identity 90.5
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
  
- Alignment No. 11923
- gi No. 2129739
- % Identity 96.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
  
- Alignment No. 11924
- gi No. 2160191
- % Identity 76.5
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
  
- Alignment No. 11925
- gi No. 2182029
- % Identity 89.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
  
- Alignment No. 11926
- gi No. 2191169
- % Identity 78.7
- Alignment Length 300
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
  
- Alignment No. 11927
- gi No. 2398519
- % Identity 82.5
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
  
- Alignment No. 11928
- gi No. 2569931
- % Identity 74.1
- Alignment Length 290
- Location of Alignment in SEQ ID NO 1366: from 1 to 220
  
- Alignment No. 11929
- gi No. 2569950
- % Identity 79.9
- Alignment Length 284
- Location of Alignment in SEQ ID NO 1366: from 1 to 214
  
- Alignment No. 11930
- gi No. 2598601

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- % Identity 77.9
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
  
- Alignment No. 11931
- gi No. 2598603
- % Identity 78.6
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
  
- Alignment No. 11932
- gi No. 2641994
- % Identity 70.8
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 214
  
- Alignment No. 11933
- gi No. 2911533
- % Identity 79.6
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
  
- Alignment No. 11934
- gi No. 3201623
- % Identity 91.2
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
  
- Alignment No. 11935
- gi No. 3236115
- % Identity 81.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
  
- Alignment No. 11936
- gi No. 3236117
- % Identity 80
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
  
- Alignment No. 11937
- gi No. 3250738
- % Identity 73.7
- Alignment Length 293
- Location of Alignment in SEQ ID NO 1366: from 1 to 220
  
- Alignment No. 11938
- gi No. 3264607
- % Identity 81.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1366: from 146 to 215
  
- Alignment No. 11939
- gi No. 3702608
- % Identity 77.2
- Alignment Length 290
- Location of Alignment in SEQ ID NO 1366: from 1 to 220
  
- Alignment No. 11940
- gi No. 3928148
- % Identity 81.6

- Alignment Length 266
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
  
- Alignment No. 11941
- gi No. 402652
- % Identity 70.9
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
  
- Alignment No. 11942
- gi No. 4140287
- % Identity 71.6
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
  
- Alignment No. 11943
- gi No. 4504163
- % Identity 70.9
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
  
- Alignment No. 11944
- gi No. 4539390
- % Identity 100
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
  
- Alignment No. 11945
- gi No. 5070700
- % Identity 70.9
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1366: from 1 to 215

Maximum Length Sequence corresponding to clone ID 256152

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1367
- Ceres seq\_id 1500109

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1368
- Ceres seq\_id 1500110
- Location of start within SEQ ID NO 1367: at 416 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 11946
- gi No. 3386609
- % Identity 99.7
- Alignment Length 348
- Location of Alignment in SEQ ID NO 1368: from 1 to 348

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1369
- Ceres seq\_id 1500111
- Location of start within SEQ ID NO 1367: at 434 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 11947
- gi No. 3386609



- % Identity 99.7
- Alignment Length 348
- Location of Alignment in SEQ ID NO 1369: from 1 to 342

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1370
- Ceres seq\_id 1500112
- Location of start within SEQ ID NO 1367: at 668 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 11948
- gi No. 3386609
- % Identity 99.7
- Alignment Length 348
- Location of Alignment in SEQ ID NO 1370: from 1 to 264

Maximum Length Sequence corresponding to clone ID 256433

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1371
- Ceres seq\_id 1500115

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1372
- Ceres seq\_id 1500116
- Location of start within SEQ ID NO 1371: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11949
- Iron/Ascorbate oxidoreductase family
- Location within SEQ ID NO 1372: from 82 to 185 aa.

(D) Related Amino Acid Sequences

- Alignment No. 11950
- gi No. 3335372
- % Identity 89.8
- Alignment Length 176
- Location of Alignment in SEQ ID NO 1372: from 29 to 185

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1373
- Ceres seq\_id 1500117
- Location of start within SEQ ID NO 1371: at 85 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11951
- Iron/Ascorbate oxidoreductase family
- Location within SEQ ID NO 1373: from 54 to 157 aa.

(D) Related Amino Acid Sequences

- Alignment No. 11952
- gi No. 3335372
- % Identity 89.8
- Alignment Length 176
- Location of Alignment in SEQ ID NO 1373: from 1 to 157

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1374
- Ceres seq\_id 1500118

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- Location of start within SEQ ID NO 1371: at 662 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11953
- Iron/Ascorbate oxidoreductase family
- Location within SEQ ID NO 1374: from 1 to 126 aa.

(D) Related Amino Acid Sequences

- Alignment No. 11954
- gi No. 3335372
- % Identity 99.5
- Alignment Length 200
- Location of Alignment in SEQ ID NO 1374: from 1 to 161

Maximum Length Sequence corresponding to clone ID 256780

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1375
- Ceres seq\_id 1500131

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1376
- Ceres seq\_id 1500132
- Location of start within SEQ ID NO 1375: at 87 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 11955
- gi No. 136739
- % Identity 83.3
- Alignment Length 468
- Location of Alignment in SEQ ID NO 1376: from 3 to 469

- Alignment No. 11956
- gi No. 1388021
- % Identity 82.1
- Alignment Length 476
- Location of Alignment in SEQ ID NO 1376: from 1 to 469

- Alignment No. 11957
- gi No. 2117937
- % Identity 81.6
- Alignment Length 467
- Location of Alignment in SEQ ID NO 1376: from 3 to 469

- Alignment No. 11958
- gi No. 3107931
- % Identity 81.7
- Alignment Length 469
- Location of Alignment in SEQ ID NO 1376: from 2 to 469

- Alignment No. 11959
- gi No. 322794
- % Identity 82.9
- Alignment Length 468
- Location of Alignment in SEQ ID NO 1376: from 3 to 469

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1377
- Ceres seq\_id 1500133
- Location of start within SEQ ID NO 1375: at 147 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 11960
- gi No. 136739
- % Identity 83.3
- Alignment Length 468
- Location of Alignment in SEQ ID NO 1377: from 1 to 449
  
- Alignment No. 11961
- gi No. 1388021
- % Identity 82.1
- Alignment Length 476
- Location of Alignment in SEQ ID NO 1377: from 1 to 449
  
- Alignment No. 11962
- gi No. 2117937
- % Identity 81.6
- Alignment Length 467
- Location of Alignment in SEQ ID NO 1377: from 1 to 449
  
- Alignment No. 11963
- gi No. 3107931
- % Identity 81.7
- Alignment Length 469
- Location of Alignment in SEQ ID NO 1377: from 1 to 449
  
- Alignment No. 11964
- gi No. 322794
- % Identity 82.9
- Alignment Length 468
- Location of Alignment in SEQ ID NO 1377: from 1 to 449

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1378
- Ceres seq\_id 1500134
- Location of start within SEQ ID NO 1375: at 273 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 11965
- gi No. 136739
- % Identity 83.3
- Alignment Length 468
- Location of Alignment in SEQ ID NO 1378: from 1 to 407
  
- Alignment No. 11966
- gi No. 1388021
- % Identity 82.1
- Alignment Length 476
- Location of Alignment in SEQ ID NO 1378: from 1 to 407
  
- Alignment No. 11967
- gi No. 2117937
- % Identity 81.6
- Alignment Length 467
- Location of Alignment in SEQ ID NO 1378: from 1 to 407
  
- Alignment No. 11968

- gi No. 3107931
- % Identity 81.7
- Alignment Length 469
- Location of Alignment in SEQ ID NO 1378: from 1 to 407
- Alignment No. 11969
- gi No. 322794
- % Identity 82.9
- Alignment Length 468
- Location of Alignment in SEQ ID NO 1378: from 1 to 407

Maximum Length Sequence corresponding to clone ID 257053

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1379
- Ceres seq\_id 1500135

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1380
- Ceres seq\_id 1500136
- Location of start within SEQ ID NO 1379: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11970
- Zinc finger, C3HC4 type (RING finger)
- Location within SEQ ID NO 1380: from 267 to 301 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1381
- Ceres seq\_id 1500137
- Location of start within SEQ ID NO 1379: at 7 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11971
- Zinc finger, C3HC4 type (RING finger)
- Location within SEQ ID NO 1381: from 265 to 299 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1382
- Ceres seq\_id 1500138
- Location of start within SEQ ID NO 1379: at 136 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11972
- Zinc finger, C3HC4 type (RING finger)
- Location within SEQ ID NO 1382: from 222 to 256 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 257278

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1383
- Ceres seq\_id 1500149

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1384
- Ceres seq\_id 1500150

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- Location of start within SEQ ID NO 1383: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1385
- Ceres seq\_id 1500151
- Location of start within SEQ ID NO 1383: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1386
- Ceres seq\_id 1500152
- Location of start within SEQ ID NO 1383: at 230 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 11973
- gi No. 3717946
- % Identity 72.6
- Alignment Length 84
- Location of Alignment in SEQ ID NO 1386: from 3 to 86
- Alignment No. 11974
- gi No. 3717987
- % Identity 76.2
- Alignment Length 84
- Location of Alignment in SEQ ID NO 1386: from 3 to 86
- Alignment No. 11975
- gi No. 3717989
- % Identity 72.6
- Alignment Length 84
- Location of Alignment in SEQ ID NO 1386: from 3 to 86

Maximum Length Sequence corresponding to clone ID 257311

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1387
- Ceres seq\_id 1500153

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1388
- Ceres seq\_id 1500154
- Location of start within SEQ ID NO 1387: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1389
- Ceres seq\_id 1500155
- Location of start within SEQ ID NO 1387: at 272 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

257311

- (D) Related Amino Acid Sequences
  - Alignment No. 11976
  - gi No. 3834307
  - % Identity 70
  - Alignment Length 40
  - Location of Alignment in SEQ ID NO 1389: from 18 to 57

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1390
  - Ceres seq\_id 1500156
  - Location of start within SEQ ID NO 1387: at 323 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
  - Alignment No. 11977
  - gi No. 3834307
  - % Identity 70
  - Alignment Length 40
  - Location of Alignment in SEQ ID NO 1390: from 1 to 40

Maximum Length Sequence corresponding to clone ID 257315

- (A) Polynucleotide Sequence
  - Pat. Appln. SEQ ID NO 1391
  - Ceres seq\_id 1500157
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1392
  - Ceres seq\_id 1500158
  - Location of start within SEQ ID NO 1391: at 264 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
  - Alignment No. 11978
  - gi No. 3335359
  - % Identity 70.2
  - Alignment Length 131
  - Location of Alignment in SEQ ID NO 1392: from 1 to 85

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1393
  - Ceres seq\_id 1500159
  - Location of start within SEQ ID NO 1391: at 291 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
  - Alignment No. 11979
  - gi No. 3335359
  - % Identity 70.2
  - Alignment Length 131
  - Location of Alignment in SEQ ID NO 1393: from 1 to 76

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1394
  - Ceres seq\_id 1500160
  - Location of start within SEQ ID NO 1391: at 351 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences

- Alignment No. 11980
- gi No. 3335359
- % Identity 70.2
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1394: from 1 to 56

Maximum Length Sequence corresponding to clone ID 257348

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1395
- Ceres seq\_id 1500165

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1396
- Ceres seq\_id 1500166
- Location of start within SEQ ID NO 1395: at 285 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11981
- Peptidyl-prolyl cis-trans isomerase
- Location within SEQ ID NO 1396: from 5 to 73 aa.

(D) Related Amino Acid Sequences

- Alignment No. 11982
- gi No. 1045518
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 1396: from 22 to 73
- Alignment No. 11983
- gi No. 1076366
- % Identity 77
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
- Alignment No. 11984
- gi No. 1076367
- % Identity 78.4
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
- Alignment No. 11985
- gi No. 1076510
- % Identity 81.1
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
- Alignment No. 11986
- gi No. 1084454
- % Identity 77.8
- Alignment Length 72
- Location of Alignment in SEQ ID NO 1396: from 3 to 73
- Alignment No. 11987
- gi No. 1084455
- % Identity 93.2
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
- Alignment No. 11988
- gi No. 118099
- % Identity 73.2

- Alignment Length 71
- Location of Alignment in SEQ ID NO 1396: from 4 to 73
  
- Alignment No. 11989
- gi No. 118103
- % Identity 86.5
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
  
- Alignment No. 11990
- gi No. 118104
- % Identity 100
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
  
- Alignment No. 11991
- gi No. 1279366
- % Identity 80
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1396: from 50 to 73
  
- Alignment No. 11992
- gi No. 1345921
- % Identity 82.4
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
  
- Alignment No. 11993
- gi No. 1480461
- % Identity 74.3
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
  
- Alignment No. 11994
- gi No. 1480463
- % Identity 74.3
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
  
- Alignment No. 11995
- gi No. 1480465
- % Identity 82.4
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
  
- Alignment No. 11996
- gi No. 1561575
- % Identity 83.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
  
- Alignment No. 11997
- gi No. 1563719
- % Identity 86.5
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
  
- Alignment No. 11998
- gi No. 1652923
- % Identity 75.7
- Alignment Length 70



- Location of Alignment in SEQ ID NO 1396: from 5 to 73
- Alignment No. 11999
- gi No. 167138
- % Identity 83.1
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1396: from 4 to 73
- Alignment No. 12000
- gi No. 1703696
- % Identity 71.6
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
- Alignment No. 12001
- gi No. 1706247
- % Identity 73
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
- Alignment No. 12002
- gi No. 1706248
- % Identity 73
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
- Alignment No. 12003
- gi No. 1706253
- % Identity 81.1
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
- Alignment No. 12004
- gi No. 1706258
- % Identity 73
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
- Alignment No. 12005
- gi No. 1928939
- % Identity 87.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
- Alignment No. 12006
- gi No. 2129568
- % Identity 71.6
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
- Alignment No. 12007
- gi No. 2129569
- % Identity 81.9
- Alignment Length 72
- Location of Alignment in SEQ ID NO 1396: from 3 to 73
- Alignment No. 12008
- gi No. 227879
- % Identity 80.5
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1396: from 1 to 73

- Alignment No. 12009
- gi No. 2443755
- % Identity 72.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1396: from 5 to 73
  
- Alignment No. 12010
- gi No. 2443757
- % Identity 82.2
- Alignment Length 73
- Location of Alignment in SEQ ID NO 1396: from 2 to 73
  
- Alignment No. 12011
- gi No. 2655157
- % Identity 73.2
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1396: from 4 to 73
  
- Alignment No. 12012
- gi No. 2655159
- % Identity 73.2
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1396: from 4 to 73
  
- Alignment No. 12013
- gi No. 2760537
- % Identity 83.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
  
- Alignment No. 12014
- gi No. 2959712
- % Identity 83.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
  
- Alignment No. 12015
- gi No. 3063396
- % Identity 79.7
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
  
- Alignment No. 12016
- gi No. 3334157
- % Identity 82.4
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
  
- Alignment No. 12017
- gi No. 3420055
- % Identity 72.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1396: from 5 to 73
  
- Alignment No. 12018
- gi No. 348725
- % Identity 72.5
- Alignment Length 51
- Location of Alignment in SEQ ID NO 1396: from 25 to 73

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- Alignment No. 12019
- gi No. 3550686
- % Identity 70.1
- Alignment Length 87
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
  
- Alignment No. 12020
- gi No. 3881310
- % Identity 81.1
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
  
- Alignment No. 12021
- gi No. 3881755
- % Identity 75.7
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
  
- Alignment No. 12022
- gi No. 4097889
- % Identity 70.4
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1396: from 5 to 73
  
- Alignment No. 12023
- gi No. 4559302
- % Identity 87.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
  
- Alignment No. 12024
- gi No. 4589980
- % Identity 81.9
- Alignment Length 72
- Location of Alignment in SEQ ID NO 1396: from 3 to 73
  
- Alignment No. 12025
- gi No. 461902
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 1396: from 22 to 73
  
- Alignment No. 12026
- gi No. 461903
- % Identity 78.4
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
  
- Alignment No. 12027
- gi No. 4803930
- % Identity 82.2
- Alignment Length 73
- Location of Alignment in SEQ ID NO 1396: from 2 to 73
  
- Alignment No. 12028
- gi No. 544125
- % Identity 76.5
- Alignment Length 68
- Location of Alignment in SEQ ID NO 1396: from 7 to 73
  
- Alignment No. 12029

- gi No. 600769
- % Identity 93.2
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
  
- Alignment No. 12030
- gi No. 630464
- % Identity 73.3
- Alignment Length 75
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
  
- Alignment No. 12031
- gi No. 68406
- % Identity 87.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
  
- Alignment No. 12032
- gi No. 68407
- % Identity 83.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
  
- Alignment No. 12033
- gi No. 939726
- % Identity 71.6
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1397
- Ceres seq\_id 1500167
- Location of start within SEQ ID NO 1395: at 312 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12034
- Peptidyl-prolyl cis-trans isomerase
- Location within SEQ ID NO 1397: from 1 to 64 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12035
- gi No. 1045518
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 1397: from 13 to 64
  
- Alignment No. 12036
- gi No. 1076366
- % Identity 77
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
  
- Alignment No. 12037
- gi No. 1076367
- % Identity 78.4
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
  
- Alignment No. 12038
- gi No. 1076510

- % Identity 81.1
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
  
- Alignment No. 12039
- gi No. 1084454
- % Identity 77.8
- Alignment Length 72
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
  
- Alignment No. 12040
- gi No. 1084455
- % Identity 93.2
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
  
- Alignment No. 12041
- gi No. 118099
- % Identity 73.2
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
  
- Alignment No. 12042
- gi No. 118103
- % Identity 86.5
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
  
- Alignment No. 12043
- gi No. 118104
- % Identity 100
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
  
- Alignment No. 12044
- gi No. 1279366
- % Identity 80
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1397: from 41 to 64
  
- Alignment No. 12045
- gi No. 1345921
- % Identity 82.4
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
  
- Alignment No. 12046
- gi No. 1480461
- % Identity 74.3
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
  
- Alignment No. 12047
- gi No. 1480463
- % Identity 74.3
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
  
- Alignment No. 12048
- gi No. 1480465
- % Identity 82.4

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- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
- Alignment No. 12049
- gi No. 1561575
- % Identity 83.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
- Alignment No. 12050
- gi No. 1563719
- % Identity 86.5
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
- Alignment No. 12051
- gi No. 1652923
- % Identity 75.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
- Alignment No. 12052
- gi No. 167138
- % Identity 83.1
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
- Alignment No. 12053
- gi No. 1703696
- % Identity 71.6
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
- Alignment No. 12054
- gi No. 1706247
- % Identity 73
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
- Alignment No. 12055
- gi No. 1706248
- % Identity 73
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
- Alignment No. 12056
- gi No. 1706253
- % Identity 81.1
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
- Alignment No. 12057
- gi No. 1706258
- % Identity 73
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
- Alignment No. 12058
- gi No. 1928939
- % Identity 87.8
- Alignment Length 74

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- Location of Alignment in SEQ ID NO 1397: from 1 to 64
- Alignment No. 12059
- gi No. 2129568
- % Identity 71.6
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
- Alignment No. 12060
- gi No. 2129569
- % Identity 81.9
- Alignment Length 72
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
- Alignment No. 12061
- gi No. 227879
- % Identity 80.5
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
- Alignment No. 12062
- gi No. 2443755
- % Identity 72.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
- Alignment No. 12063
- gi No. 2443757
- % Identity 82.2
- Alignment Length 73
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
- Alignment No. 12064
- gi No. 2655157
- % Identity 73.2
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
- Alignment No. 12065
- gi No. 2655159
- % Identity 73.2
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
- Alignment No. 12066
- gi No. 2760537
- % Identity 83.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
- Alignment No. 12067
- gi No. 2959712
- % Identity 83.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
- Alignment No. 12068
- gi No. 3063396
- % Identity 79.7
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64

- Alignment No. 12069
- gi No. 3334157
- % Identity 82.4
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
  
- Alignment No. 12070
- gi No. 3420055
- % Identity 72.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
  
- Alignment No. 12071
- gi No. 348725
- % Identity 72.5
- Alignment Length 51
- Location of Alignment in SEQ ID NO 1397: from 16 to 64
  
- Alignment No. 12072
- gi No. 3550686
- % Identity 70.1
- Alignment Length 87
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
  
- Alignment No. 12073
- gi No. 3881310
- % Identity 81.1
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
  
- Alignment No. 12074
- gi No. 3881755
- % Identity 75.7
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
  
- Alignment No. 12075
- gi No. 4097889
- % Identity 70.4
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
  
- Alignment No. 12076
- gi No. 4559302
- % Identity 87.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
  
- Alignment No. 12077
- gi No. 4589980
- % Identity 81.9
- Alignment Length 72
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
  
- Alignment No. 12078
- gi No. 461902
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 1397: from 13 to 64

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(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences  
- Alignment No. 12088

- gi No. 1045518
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12089
- gi No. 1076366
- % Identity 77
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12090
- gi No. 1076367
- % Identity 78.4
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12091
- gi No. 1076510
- % Identity 81.1
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12092
- gi No. 1084454
- % Identity 77.8
- Alignment Length 72
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12093
- gi No. 1084455
- % Identity 93.2
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12094
- gi No. 118099
- % Identity 73.2
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12095
- gi No. 118103
- % Identity 86.5
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12096
- gi No. 118104
- % Identity 100
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12097
- gi No. 1279366
- % Identity 80
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1398: from 29 to 52
  
- Alignment No. 12098
- gi No. 1345921

- % Identity 82.4
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12099
- gi No. 1480461
- % Identity 74.3
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12100
- gi No. 1480463
- % Identity 74.3
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12101
- gi No. 1480465
- % Identity 82.4
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12102
- gi No. 1561575
- % Identity 83.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12103
- gi No. 1563719
- % Identity 86.5
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12104
- gi No. 1652923
- % Identity 75.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12105
- gi No. 167138
- % Identity 83.1
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12106
- gi No. 1703696
- % Identity 71.6
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12107
- gi No. 1706247
- % Identity 73
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12108
- gi No. 1706248
- % Identity 73

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- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12109
- gi No. 1706253
- % Identity 81.1
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12110
- gi No. 1706258
- % Identity 73
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12111
- gi No. 1928939
- % Identity 87.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12112
- gi No. 2129568
- % Identity 71.6
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12113
- gi No. 2129569
- % Identity 81.9
- Alignment Length 72
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12114
- gi No. 227879
- % Identity 80.5
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12115
- gi No. 2443755
- % Identity 72.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12116
- gi No. 2443757
- % Identity 82.2
- Alignment Length 73
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12117
- gi No. 2655157
- % Identity 73.2
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
  
- Alignment No. 12118
- gi No. 2655159
- % Identity 73.2
- Alignment Length 71

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- Location of Alignment in SEQ ID NO 1398: from 1 to 52
- Alignment No. 12119
- gi No. 2760537
- % Identity 83.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
- Alignment No. 12120
- gi No. 2959712
- % Identity 83.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
- Alignment No. 12121
- gi No. 3063396
- % Identity 79.7
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
- Alignment No. 12122
- gi No. 3334157
- % Identity 82.4
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
- Alignment No. 12123
- gi No. 3420055
- % Identity 72.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
- Alignment No. 12124
- gi No. 348725
- % Identity 72.5
- Alignment Length 51
- Location of Alignment in SEQ ID NO 1398: from 4 to 52
- Alignment No. 12125
- gi No. 3550686
- % Identity 70.1
- Alignment Length 87
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
- Alignment No. 12126
- gi No. 3881310
- % Identity 81.1
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
- Alignment No. 12127
- gi No. 3881755
- % Identity 75.7
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
- Alignment No. 12128
- gi No. 4097889
- % Identity 70.4
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1398: from 1 to 52

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- Alignment No. 12129
- gi No. 4559302
- % Identity 87.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
- Alignment No. 12130
- gi No. 4589980
- % Identity 81.9
- Alignment Length 72
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
- Alignment No. 12131
- gi No. 461902
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
- Alignment No. 12132
- gi No. 461903
- % Identity 78.4
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
- Alignment No. 12133
- gi No. 4803930
- % Identity 82.2
- Alignment Length 73
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
- Alignment No. 12134
- gi No. 544125
- % Identity 76.5
- Alignment Length 68
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
- Alignment No. 12135
- gi No. 600769
- % Identity 93.2
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
- Alignment No. 12136
- gi No. 630464
- % Identity 73.3
- Alignment Length 75
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
- Alignment No. 12137
- gi No. 68406
- % Identity 87.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
- Alignment No. 12138
- gi No. 68407
- % Identity 83.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52

- Alignment No. 12139
- gi No. 939726
- % Identity 71.6
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52

Maximum Length Sequence corresponding to clone ID 257355

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1399
- Ceres seq\_id 1500169

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1400
- Ceres seq\_id 1500170
- Location of start within SEQ ID NO 1399: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12140
- ATPases associated with various cellular activities (AAA)
- Location within SEQ ID NO 1400: from 117 to 168 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 257369

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1401
- Ceres seq\_id 1500179

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1402
- Ceres seq\_id 1500180
- Location of start within SEQ ID NO 1401: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1403
- Ceres seq\_id 1500181
- Location of start within SEQ ID NO 1401: at 67 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12141
- gi No. 2642158
- % Identity 70.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1403: from 11 to 155
  
- Alignment No. 12142
- gi No. 81286
- % Identity 71.4
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1403: from 4 to 17

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1404
- Ceres seq\_id 1500182
- Location of start within SEQ ID NO 1401: at 181 nt.

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(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12143
- gi No. 2642158
- % Identity 70.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1404: from 1 to 117

Maximum Length Sequence corresponding to clone ID 257391

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1405
- Ceres seq\_id 1500186

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1406
- Ceres seq\_id 1500187
- Location of start within SEQ ID NO 1405: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12144
- Syntaxin
- Location within SEQ ID NO 1406: from 51 to 178 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1407
- Ceres seq\_id 1500188
- Location of start within SEQ ID NO 1405: at 92 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12145
- Syntaxin
- Location within SEQ ID NO 1407: from 21 to 148 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1408
- Ceres seq\_id 1500189
- Location of start within SEQ ID NO 1405: at 161 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12146
- Syntaxin
- Location within SEQ ID NO 1408: from 1 to 125 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 257556

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1409
- Ceres seq\_id 1500190

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1410
- Ceres seq\_id 1500191
- Location of start within SEQ ID NO 1409: at 3 nt.



(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12147
- CTF/NF-I family
- Location within SEQ ID NO 1410: from 32 to 107 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12148
- gi No. 1914853
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1410: from 166 to 176
- Alignment No. 12149
- gi No. 3650031
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1410: from 163 to 173
- Alignment No. 12150
- gi No. 5420387
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1410: from 290 to 300

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1411
- Ceres seq\_id 1500192
- Location of start within SEQ ID NO 1409: at 21 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12151
- CTF/NF-I family
- Location within SEQ ID NO 1411: from 26 to 101 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12152
- gi No. 1914853
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1411: from 160 to 170
- Alignment No. 12153
- gi No. 3650031
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1411: from 157 to 167
- Alignment No. 12154
- gi No. 5420387
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1411: from 284 to 294

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1412
- Ceres seq\_id 1500193
- Location of start within SEQ ID NO 1409: at 612 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12155
- gi No. 5420387
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1412: from 87 to 97

Maximum Length Sequence corresponding to clone ID 257654

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1413
- Ceres seq\_id 1500198

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1414
- Ceres seq\_id 1500199
- Location of start within SEQ ID NO 1413: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1415
- Ceres seq\_id 1500200
- Location of start within SEQ ID NO 1413: at 245 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12156
- SRF-type transcription factor (DNA-binding and dimerisation domain)
- Location within SEQ ID NO 1415: from 1 to 59 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12157
- gi No. 1001935
- % Identity 74.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1415: from 1 to 70
- Alignment No. 12158
- gi No. 1049022
- % Identity 74.1
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1415: from 1 to 85
- Alignment No. 12159
- gi No. 1076646
- % Identity 73.9
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1415: from 1 to 85
- Alignment No. 12160
- gi No. 1076827
- % Identity 72.9
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1415: from 1 to 58
- Alignment No. 12161
- gi No. 1206003

- % Identity 71.8
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1415: from 1 to 70
  
- Alignment No. 12162
- gi No. 1208800
- % Identity 76
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1415: from 17 to 41
  
- Alignment No. 12163
- gi No. 1208802
- % Identity 84
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1415: from 17 to 41
  
- Alignment No. 12164
- gi No. 1208804
- % Identity 82.6
- Alignment Length 23
- Location of Alignment in SEQ ID NO 1415: from 19 to 41
  
- Alignment No. 12165
- gi No. 1239961
- % Identity 71.8
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1415: from 1 to 70
  
- Alignment No. 12166
- gi No. 1345965
- % Identity 70.4
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1415: from 1 to 70
  
- Alignment No. 12167
- gi No. 1362195
- % Identity 75.4
- Alignment Length 57
- Location of Alignment in SEQ ID NO 1415: from 3 to 59
  
- Alignment No. 12168
- gi No. 1362196
- % Identity 78.9
- Alignment Length 57
- Location of Alignment in SEQ ID NO 1415: from 3 to 59
  
- Alignment No. 12169
- gi No. 1362197
- % Identity 75.4
- Alignment Length 57
- Location of Alignment in SEQ ID NO 1415: from 3 to 59
  
- Alignment No. 12170
- gi No. 1362198
- % Identity 77.2
- Alignment Length 57
- Location of Alignment in SEQ ID NO 1415: from 3 to 59
  
- Alignment No. 12171
- gi No. 1362199
- % Identity 76.3

- Alignment Length 59
- Location of Alignment in SEQ ID NO 1415: from 1 to 59
  
- Alignment No. 12172
- gi No. 1362200
- % Identity 78
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1415: from 1 to 59
  
- Alignment No. 12173
- gi No. 1362201
- % Identity 84.4
- Alignment Length 45
- Location of Alignment in SEQ ID NO 1415: from 15 to 59
  
- Alignment No. 12174
- gi No. 1362202
- % Identity 77.3
- Alignment Length 44
- Location of Alignment in SEQ ID NO 1415: from 16 to 59
  
- Alignment No. 12175
- gi No. 1362203
- % Identity 71.2
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1415: from 1 to 59
  
- Alignment No. 12176
- gi No. 1362204
- % Identity 81.8
- Alignment Length 44
- Location of Alignment in SEQ ID NO 1415: from 16 to 59
  
- Alignment No. 12177
- gi No. 1362205
- % Identity 82.2
- Alignment Length 45
- Location of Alignment in SEQ ID NO 1415: from 16 to 60
  
- Alignment No. 12178
- gi No. 1362206
- % Identity 77.3
- Alignment Length 44
- Location of Alignment in SEQ ID NO 1415: from 16 to 59
  
- Alignment No. 12179
- gi No. 1362209
- % Identity 73.3
- Alignment Length 60
- Location of Alignment in SEQ ID NO 1415: from 1 to 59
  
- Alignment No. 12180
- gi No. 2160701
- % Identity 75.4
- Alignment Length 69
- Location of Alignment in SEQ ID NO 1415: from 1 to 69
  
- Alignment No. 12181
- gi No. 2286109
- % Identity 71.4
- Alignment Length 70

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- Location of Alignment in SEQ ID NO 1415: from 1 to 70
- Alignment No. 12182
- gi No. 2459835
- % Identity 71.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1415: from 1 to 56
- Alignment No. 12183
- gi No. 2463333
- % Identity 70.4
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1415: from 1 to 70
- Alignment No. 12184
- gi No. 2979566
- % Identity 75.3
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1415: from 1 to 85
- Alignment No. 12185
- gi No. 3023536
- % Identity 71.8
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1415: from 1 to 70
- Alignment No. 12186
- gi No. 3114588
- % Identity 71.8
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1415: from 1 to 70
- Alignment No. 12187
- gi No. 320596
- % Identity 70.4
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1415: from 1 to 70
- Alignment No. 12188
- gi No. 322801
- % Identity 70.1
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1415: from 3 to 79
- Alignment No. 12189
- gi No. 3292820
- % Identity 71.8
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1415: from 1 to 85
- Alignment No. 12190
- gi No. 3493647
- % Identity 80.2
- Alignment Length 81
- Location of Alignment in SEQ ID NO 1415: from 1 to 81
- Alignment No. 12191
- gi No. 3646322
- % Identity 75
- Alignment Length 68
- Location of Alignment in SEQ ID NO 1415: from 4 to 70

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- [illegible]

- Alignment No. 12202
- gi No. 497145
- % Identity 80.8
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1415: from 10 to 35

- Alignment No. 12203
- gi No. 497147
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1415: from 10 to 35

- Alignment No. 12204
- gi No. 497149
- % Identity 80.8
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1415: from 10 to 35

- Alignment No. 12205
- gi No. 5002523
- % Identity 76.3
- Alignment Length 80
- Location of Alignment in SEQ ID NO 1415: from 1 to 79

- Alignment No. 12206
- gi No. 5019431
- % Identity 72.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1415: from 1 to 76

- Alignment No. 12207
- gi No. 5031217
- % Identity 70.4
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1415: from 1 to 70

- Alignment No. 12208
- gi No. 5051933
- % Identity 81.6
- Alignment Length 87
- Location of Alignment in SEQ ID NO 1415: from 1 to 85

- Alignment No. 12209
- gi No. 5051935
- % Identity 75
- Alignment Length 60
- Location of Alignment in SEQ ID NO 1415: from 12 to 70

- Alignment No. 12210
- gi No. 5070138
- % Identity 70.4
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1415: from 1 to 70

- Alignment No. 12211
- gi No. 5295990
- % Identity 90.7
- Alignment Length 86
- Location of Alignment in SEQ ID NO 1415: from 1 to 85

- Alignment No. 12212

- gi No. 542034
- % Identity 76.6
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1415: from 1 to 77

- Alignment No. 12213
- gi No. 542192
- % Identity 75
- Alignment Length 60
- Location of Alignment in SEQ ID NO 1415: from 11 to 70

- Alignment No. 12214
- gi No. 5566279
- % Identity 82.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1415: from 12 to 51

- Alignment No. 12215
- gi No. 5712746
- % Identity 78
- Alignment Length 50
- Location of Alignment in SEQ ID NO 1415: from 7 to 56

- Alignment No. 12216
- gi No. 5712748
- % Identity 78
- Alignment Length 50
- Location of Alignment in SEQ ID NO 1415: from 7 to 56

- Alignment No. 12217
- gi No. 695686
- % Identity 75.4
- Alignment Length 69
- Location of Alignment in SEQ ID NO 1415: from 1 to 69

- Alignment No. 12218
- gi No. 695688
- % Identity 71.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1415: from 1 to 76

- Alignment No. 12219
- gi No. 695690
- % Identity 73
- Alignment Length 89
- Location of Alignment in SEQ ID NO 1415: from 1 to 85

- Alignment No. 12220
- gi No. 793906
- % Identity 73.3
- Alignment Length 60
- Location of Alignment in SEQ ID NO 1415: from 1 to 59

- Alignment No. 12221
- gi No. 81611
- % Identity 76.4
- Alignment Length 55
- Location of Alignment in SEQ ID NO 1415: from 3 to 57

- Alignment No. 12222
- gi No. 862644

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- ```
- % Identity 74.3
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1415: from 7 to 79

- Alignment No. 12223
- gi No. 939779
- % Identity 71.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1415: from 1 to 70

- Alignment No. 12224
- gi No. 939783
- % Identity 75.9
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1415: from 1 to 57

- Alignment No. 12225
- gi No. 951172
- % Identity 71.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1415: from 1 to 70
```

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1416
- Ceres seq\_id 1500201
- Location of start within SEQ ID NO 1413: at 266 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12226
- SRF-type transcription factor (DNA-binding and dimerisation domain)
- Location within SEQ ID NO 1416: from 1 to 52 aa.

#### (D) Related Amino Acid Sequences

- ```
- Alignment No. 12227
- gi No. 1001935
- % Identity 74.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1416: from 1 to 63

- Alignment No. 12228
- gi No. 1049022
- % Identity 74.1
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1416: from 1 to 78

- Alignment No. 12229
- gi No. 1076646
- % Identity 73.9
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1416: from 1 to 78

- Alignment No. 12230
- gi No. 1076827
- % Identity 72.9
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1416: from 1 to 51

- Alignment No. 12231
- gi No. 1206003
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- % Identity 71.8
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1416: from 1 to 63

- Alignment No. 12232
- gi No. 1208800
- % Identity 76
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1416: from 10 to 34

- Alignment No. 12233
- gi No. 1208802
- % Identity 84
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1416: from 10 to 34

- Alignment No. 12234
- gi No. 1208804
- % Identity 82.6
- Alignment Length 23
- Location of Alignment in SEQ ID NO 1416: from 12 to 34

- Alignment No. 12235
- gi No. 1239961
- % Identity 71.8
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1416: from 1 to 63

- Alignment No. 12236
- gi No. 1345965
- % Identity 70.4
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1416: from 1 to 63

- Alignment No. 12237
- gi No. 1362195
- % Identity 75.4
- Alignment Length 57
- Location of Alignment in SEQ ID NO 1416: from 1 to 52

- Alignment No. 12238
- gi No. 1362196
- % Identity 78.9
- Alignment Length 57
- Location of Alignment in SEQ ID NO 1416: from 1 to 52

- Alignment No. 12239
- gi No. 1362197
- % Identity 75.4
- Alignment Length 57
- Location of Alignment in SEQ ID NO 1416: from 1 to 52

- Alignment No. 12240
- gi No. 1362198
- % Identity 77.2
- Alignment Length 57
- Location of Alignment in SEQ ID NO 1416: from 1 to 52

- Alignment No. 12241
- gi No. 1362199
- % Identity 76.3

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- Alignment Length 59
- Location of Alignment in SEQ ID NO 1416: from 1 to 52
  
- Alignment No. 12242
- gi No. 1362200
- % Identity 78
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1416: from 1 to 52
  
- Alignment No. 12243
- gi No. 1362201
- % Identity 84.4
- Alignment Length 45
- Location of Alignment in SEQ ID NO 1416: from 8 to 52
  
- Alignment No. 12244
- gi No. 1362202
- % Identity 77.3
- Alignment Length 44
- Location of Alignment in SEQ ID NO 1416: from 9 to 52
  
- Alignment No. 12245
- gi No. 1362203
- % Identity 71.2
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1416: from 1 to 52
  
- Alignment No. 12246
- gi No. 1362204
- % Identity 81.8
- Alignment Length 44
- Location of Alignment in SEQ ID NO 1416: from 9 to 52
  
- Alignment No. 12247
- gi No. 1362205
- % Identity 82.2
- Alignment Length 45
- Location of Alignment in SEQ ID NO 1416: from 9 to 53
  
- Alignment No. 12248
- gi No. 1362206
- % Identity 77.3
- Alignment Length 44
- Location of Alignment in SEQ ID NO 1416: from 9 to 52
  
- Alignment No. 12249
- gi No. 1362209
- % Identity 73.3
- Alignment Length 60
- Location of Alignment in SEQ ID NO 1416: from 1 to 52
  
- Alignment No. 12250
- gi No. 2160701
- % Identity 75.4
- Alignment Length 69
- Location of Alignment in SEQ ID NO 1416: from 1 to 62
  
- Alignment No. 12251
- gi No. 2286109
- % Identity 71.4
- Alignment Length 70

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- Location of Alignment in SEQ ID NO 1416: from 1 to 63
- Alignment No. 12252
- gi No. 2459835
- % Identity 71.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1416: from 1 to 49
- Alignment No. 12253
- gi No. 2463333
- % Identity 70.4
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1416: from 1 to 63
- Alignment No. 12254
- gi No. 2979566
- % Identity 75.3
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1416: from 1 to 78
- Alignment No. 12255
- gi No. 3023536
- % Identity 71.8
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1416: from 1 to 63
- Alignment No. 12256
- gi No. 3114588
- % Identity 71.8
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1416: from 1 to 63
- Alignment No. 12257
- gi No. 320596
- % Identity 70.4
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1416: from 1 to 63
- Alignment No. 12258
- gi No. 322801
- % Identity 70.1
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1416: from 1 to 72
- Alignment No. 12259
- gi No. 3292820
- % Identity 71.8
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1416: from 1 to 78
- Alignment No. 12260
- gi No. 3493647
- % Identity 80.2
- Alignment Length 81
- Location of Alignment in SEQ ID NO 1416: from 1 to 74
- Alignment No. 12261
- gi No. 3646322
- % Identity 75
- Alignment Length 68
- Location of Alignment in SEQ ID NO 1416: from 1 to 63

- Alignment No. 12262
- gi No. 3646340
- % Identity 71.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1416: from 1 to 63
  
- Alignment No. 12263
- gi No. 3688591
- % Identity 71.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1416: from 1 to 63
  
- Alignment No. 12264
- gi No. 3851331
- % Identity 71.9
- Alignment Length 57
- Location of Alignment in SEQ ID NO 1416: from 9 to 64
  
- Alignment No. 12265
- gi No. 3851333
- % Identity 78.2
- Alignment Length 55
- Location of Alignment in SEQ ID NO 1416: from 9 to 62
  
- Alignment No. 12266
- gi No. 4033710
- % Identity 71.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1416: from 1 to 69
  
- Alignment No. 12267
- gi No. 4033721
- % Identity 71.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1416: from 1 to 69
  
- Alignment No. 12268
- gi No. 4033725
- % Identity 70.8
- Alignment Length 72
- Location of Alignment in SEQ ID NO 1416: from 1 to 69
  
- Alignment No. 12269
- gi No. 4101710
- % Identity 71.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1416: from 1 to 69
  
- Alignment No. 12270
- gi No. 4103486
- % Identity 71.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1416: from 1 to 69
  
- Alignment No. 12271
- gi No. 4322475
- % Identity 77.1
- Alignment Length 83
- Location of Alignment in SEQ ID NO 1416: from 1 to 76

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- Alignment No. 12272
- gi No. 497145
- % Identity 80.8
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1416: from 3 to 28
- Alignment No. 12273
- gi No. 497147
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1416: from 3 to 28
- Alignment No. 12274
- gi No. 497149
- % Identity 80.8
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1416: from 3 to 28
- Alignment No. 12275
- gi No. 5002523
- % Identity 76.3
- Alignment Length 80
- Location of Alignment in SEQ ID NO 1416: from 1 to 72
- Alignment No. 12276
- gi No. 5019431
- % Identity 72.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1416: from 1 to 69
- Alignment No. 12277
- gi No. 5031217
- % Identity 70.4
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1416: from 1 to 63
- Alignment No. 12278
- gi No. 5051933
- % Identity 81.6
- Alignment Length 87
- Location of Alignment in SEQ ID NO 1416: from 1 to 78
- Alignment No. 12279
- gi No. 5051935
- % Identity 75
- Alignment Length 60
- Location of Alignment in SEQ ID NO 1416: from 5 to 63
- Alignment No. 12280
- gi No. 5070138
- % Identity 70.4
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1416: from 1 to 63
- Alignment No. 12281
- gi No. 5295990
- % Identity 90.7
- Alignment Length 86
- Location of Alignment in SEQ ID NO 1416: from 1 to 78
- Alignment No. 12282

- gi No. 542034
- % Identity 76.6
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1416: from 1 to 70
  
- Alignment No. 12283
- gi No. 542192
- % Identity 75
- Alignment Length 60
- Location of Alignment in SEQ ID NO 1416: from 4 to 63
  
- Alignment No. 12284
- gi No. 5566279
- % Identity 82.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1416: from 5 to 44
  
- Alignment No. 12285
- gi No. 5712746
- % Identity 78
- Alignment Length 50
- Location of Alignment in SEQ ID NO 1416: from 1 to 49
  
- Alignment No. 12286
- gi No. 5712748
- % Identity 78
- Alignment Length 50
- Location of Alignment in SEQ ID NO 1416: from 1 to 49
  
- Alignment No. 12287
- gi No. 695686
- % Identity 75.4
- Alignment Length 69
- Location of Alignment in SEQ ID NO 1416: from 1 to 62
  
- Alignment No. 12288
- gi No. 695688
- % Identity 71.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1416: from 1 to 69
  
- Alignment No. 12289
- gi No. 695690
- % Identity 73
- Alignment Length 89
- Location of Alignment in SEQ ID NO 1416: from 1 to 78
  
- Alignment No. 12290
- gi No. 793906
- % Identity 73.3
- Alignment Length 60
- Location of Alignment in SEQ ID NO 1416: from 1 to 52
  
- Alignment No. 12291
- gi No. 81611
- % Identity 76.4
- Alignment Length 55
- Location of Alignment in SEQ ID NO 1416: from 1 to 50
  
- Alignment No. 12292
- gi No. 862644

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- % Identity 74.3
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1416: from 1 to 72
  
- Alignment No. 12293
- gi No. 939779
- % Identity 71.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1416: from 1 to 63
  
- Alignment No. 12294
- gi No. 939783
- % Identity 75.9
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1416: from 1 to 50
  
- Alignment No. 12295
- gi No. 951172
- % Identity 71.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1416: from 1 to 63

Maximum Length Sequence corresponding to clone ID 257713

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1417
- Ceres seq\_id 1500202

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1418
- Ceres seq\_id 1500203
- Location of start within SEQ ID NO 1417: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1419
- Ceres seq\_id 1500204
- Location of start within SEQ ID NO 1417: at 469 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12296
- gi No. 4680201
- % Identity 90.9
- Alignment Length 44
- Location of Alignment in SEQ ID NO 1419: from 20 to 63
  
- Alignment No. 12297
- gi No. 4680489
- % Identity 73
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1419: from 1 to 63

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1420
- Ceres seq\_id 1500205
- Location of start within SEQ ID NO 1417: at 499 nt.



(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12298
- gi No. 4680201
- % Identity 90.9
- Alignment Length 44
- Location of Alignment in SEQ ID NO 1420: from 10 to 53
  
- Alignment No. 12299
- gi No. 4680489
- % Identity 73
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1420: from 1 to 53

Maximum Length Sequence corresponding to clone ID 257780

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1421
- Ceres seq\_id 1500212

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1422
- Ceres seq\_id 1500213
- Location of start within SEQ ID NO 1421: at 351 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12300
- Ribosomal protein S17
- Location within SEQ ID NO 1422: from 1 to 57 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12301
- gi No. 1173221
- % Identity 85
- Alignment Length 133
- Location of Alignment in SEQ ID NO 1422: from 1 to 57
  
- Alignment No. 12302
- gi No. 1173223
- % Identity 88
- Alignment Length 133
- Location of Alignment in SEQ ID NO 1422: from 1 to 57
  
- Alignment No. 12303
- gi No. 133866
- % Identity 86.5
- Alignment Length 133
- Location of Alignment in SEQ ID NO 1422: from 1 to 57
  
- Alignment No. 12304
- gi No. 133867
- % Identity 92.5
- Alignment Length 133
- Location of Alignment in SEQ ID NO 1422: from 1 to 57
  
- Alignment No. 12305
- gi No. 166867
- % Identity 86.5
- Alignment Length 133
- Location of Alignment in SEQ ID NO 1422: from 1 to 57

- Alignment No. 12306
- gi No. 5708091
- % Identity 85.7
- Alignment Length 133
- Location of Alignment in SEQ ID NO 1422: from 1 to 57
- Alignment No. 12307
- gi No. 81811
- % Identity 88.2
- Alignment Length 119
- Location of Alignment in SEQ ID NO 1422: from 1 to 57

Maximum Length Sequence corresponding to clone ID 257928

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1423
- Ceres seq\_id 1500234

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1424
- Ceres seq\_id 1500235
- Location of start within SEQ ID NO 1423: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1425
- Ceres seq\_id 1500236
- Location of start within SEQ ID NO 1423: at 62 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1426
- Ceres seq\_id 1500237
- Location of start within SEQ ID NO 1423: at 201 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12308
- gi No. 2258365
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1426: from 46 to 92
- Alignment No. 12309
- gi No. 3342734
- % Identity 71.4
- Alignment Length 49
- Location of Alignment in SEQ ID NO 1426: from 44 to 92
- Alignment No. 12310
- gi No. 3860916
- % Identity 70.5
- Alignment Length 44
- Location of Alignment in SEQ ID NO 1426: from 49 to 92

Maximum Length Sequence corresponding to clone ID 257979

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- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 1427
  - Ceres seq\_id 1500246
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 1428
  - Ceres seq\_id 1500247
  - Location of start within SEQ ID NO 1427: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
- Alignment No. 12311
  - recA bacterial DNA recombination proteins
  - Location within SEQ ID NO 1428: from 104 to 154 aa.
- (D) Related Amino Acid Sequences
- Alignment No. 12312
  - gi No. 1172887
  - % Identity 72.2
  - Alignment Length 18
  - Location of Alignment in SEQ ID NO 1428: from 137 to 154
- Alignment No. 12313
  - gi No. 403968
  - % Identity 77.8
  - Alignment Length 18
  - Location of Alignment in SEQ ID NO 1428: from 136 to 153
- Alignment No. 12314
  - gi No. 464598
  - % Identity 75
  - Alignment Length 20
  - Location of Alignment in SEQ ID NO 1428: from 135 to 154
- Alignment No. 12315
  - gi No. 543677
  - % Identity 75
  - Alignment Length 20
  - Location of Alignment in SEQ ID NO 1428: from 135 to 154
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 1429
  - Ceres seq\_id 1500248
  - Location of start within SEQ ID NO 1427: at 60 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
- Alignment No. 12316
  - recA bacterial DNA recombination proteins
  - Location within SEQ ID NO 1429: from 85 to 135 aa.
- (D) Related Amino Acid Sequences
- Alignment No. 12317
  - gi No. 1172887
  - % Identity 72.2
  - Alignment Length 18
  - Location of Alignment in SEQ ID NO 1429: from 118 to 135
- Alignment No. 12318
  - gi No. 403968
  - % Identity 77.8
  - Alignment Length 18

- Location of Alignment in SEQ ID NO 1429: from 117 to 134
- Alignment No. 12319
- gi No. 464598
- % Identity 75
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1429: from 116 to 135
- Alignment No. 12320
- gi No. 543677
- % Identity 75
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1429: from 116 to 135

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1430
- Ceres seq\_id 1500249
- Location of start within SEQ ID NO 1427: at 249 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12321
- recA bacterial DNA recombination proteins
- Location within SEQ ID NO 1430: from 22 to 72 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12322
- gi No. 1172887
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1430: from 55 to 72
- Alignment No. 12323
- gi No. 403968
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1430: from 54 to 71
- Alignment No. 12324
- gi No. 464598
- % Identity 75
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1430: from 53 to 72
- Alignment No. 12325
- gi No. 543677
- % Identity 75
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1430: from 53 to 72

Maximum Length Sequence corresponding to clone ID 257985

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1431
- Ceres seq\_id 1500250

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1432
- Ceres seq\_id 1500251
- Location of start within SEQ ID NO 1431: at 160 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

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- Alignment No. 12326
- RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- Location within SEQ ID NO 1432: from 64 to 135 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12327
- gi No. 140346
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1432: from 45 to 57

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1433
- Ceres seq\_id 1500252
- Location of start within SEQ ID NO 1431: at 272 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 258340

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1434
- Ceres seq\_id 1500263

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1435
- Ceres seq\_id 1500264
- Location of start within SEQ ID NO 1434: at 209 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12328
- Syntaxin
- Location within SEQ ID NO 1435: from 5 to 306 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1436
- Ceres seq\_id 1500265
- Location of start within SEQ ID NO 1434: at 305 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12329
- Syntaxin
- Location within SEQ ID NO 1436: from 1 to 274 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1437
- Ceres seq\_id 1500266
- Location of start within SEQ ID NO 1434: at 401 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12330
- Syntaxin
- Location within SEQ ID NO 1437: from 1 to 242 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 258706

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1438
- Ceres seq\_id 1500283

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1439
- Ceres seq\_id 1500284
- Location of start within SEQ ID NO 1438: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1440
- Ceres seq\_id 1500285
- Location of start within SEQ ID NO 1438: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12331
- gi No. 5042457
- % Identity 95.5
- Alignment Length 66
- Location of Alignment in SEQ ID NO 1440: from 42 to 107

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1441
- Ceres seq\_id 1500286
- Location of start within SEQ ID NO 1438: at 125 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12332
- gi No. 5042457
- % Identity 95.5
- Alignment Length 66
- Location of Alignment in SEQ ID NO 1441: from 1 to 66

Maximum Length Sequence corresponding to clone ID 259439

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1442
- Ceres seq\_id 1500298

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1443
- Ceres seq\_id 1500299
- Location of start within SEQ ID NO 1442: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12333
- Zinc finger C-x8-C-x5-C-x3-H type (and similar).
- Location within SEQ ID NO 1443: from 30 to 55 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1444
- Ceres seq\_id 1500300
- Location of start within SEQ ID NO 1442: at 7 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12334
- Zinc finger C-x8-C-x5-C-x3-H type (and similar).
- Location within SEQ ID NO 1444: from 28 to 53 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1445
- Ceres seq\_id 1500301
- Location of start within SEQ ID NO 1442: at 106 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 259532

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1446
- Ceres seq\_id 1500305

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1447
- Ceres seq\_id 1500306
- Location of start within SEQ ID NO 1446: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12335
- DEAD/DEAH box helicase
- Location within SEQ ID NO 1447: from 95 to 166 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12336
- gi No. 1749748
- % Identity 80
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1447: from 127 to 166
- Alignment No. 12337
- gi No. 2500530
- % Identity 73
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1447: from 41 to 166
- Alignment No. 12338
- gi No. 2500531
- % Identity 74
- Alignment Length 129
- Location of Alignment in SEQ ID NO 1447: from 41 to 166
- Alignment No. 12339
- gi No. 3132829
- % Identity 73.8
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1447: from 41 to 166

- Alignment No. 12340
- gi No. 3776005
- % Identity 72.9
- Alignment Length 156
- Location of Alignment in SEQ ID NO 1447: from 15 to 166
  
- Alignment No. 12341
- gi No. 3805815
- % Identity 73.2
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1447: from 41 to 166
  
- Alignment No. 12342
- gi No. 4235116
- % Identity 74
- Alignment Length 129
- Location of Alignment in SEQ ID NO 1447: from 41 to 166
  
- Alignment No. 12343
- gi No. 4758112
- % Identity 73.2
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1447: from 41 to 166
  
- Alignment No. 12344
- gi No. 5031659
- % Identity 70.6
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1447: from 41 to 166
  
- Alignment No. 12345
- gi No. 539961
- % Identity 74
- Alignment Length 129
- Location of Alignment in SEQ ID NO 1447: from 41 to 166

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1448
- Ceres seq\_id 1500307
- Location of start within SEQ ID NO 1446: at 103 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12346
- DEAD/DEAH box helicase
- Location within SEQ ID NO 1448: from 61 to 132 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12347
- gi No. 1749748
- % Identity 80
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1448: from 93 to 132
  
- Alignment No. 12348
- gi No. 2500530
- % Identity 73
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1448: from 7 to 132
  
- Alignment No. 12349



- ```
- gi No. 2500531
- % Identity 74
- Alignment Length 129
- Location of Alignment in SEQ ID NO 1448: from 7 to 132

- Alignment No. 12350
- gi No. 3132829
- % Identity 73.8
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1448: from 7 to 132

- Alignment No. 12351
- gi No. 3776005
- % Identity 72.9
- Alignment Length 156
- Location of Alignment in SEQ ID NO 1448: from 1 to 132

- Alignment No. 12352
- gi No. 3805815
- % Identity 73.2
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1448: from 7 to 132

- Alignment No. 12353
- gi No. 4235116
- % Identity 74
- Alignment Length 129
- Location of Alignment in SEQ ID NO 1448: from 7 to 132

- Alignment No. 12354
- gi No. 4758112
- % Identity 73.2
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1448: from 7 to 132

- Alignment No. 12355
- gi No. 5031659
- % Identity 70.6
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1448: from 7 to 132

- Alignment No. 12356
- gi No. 539961
- % Identity 74
- Alignment Length 129
- Location of Alignment in SEQ ID NO 1448: from 7 to 132
```

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1449
- Ceres seq_id 1500308
- Location of start within SEQ ID NO 1446: at 106 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12357
- DEAD/DEAH box helicase
- Location within SEQ ID NO 1449: from 60 to 131 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12358
- qi No. 1749748

- % Identity 80
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1449: from 92 to 131
- Alignment No. 12359
- gi No. 2500530
- % Identity 73
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1449: from 6 to 131
- Alignment No. 12360
- gi No. 2500531
- % Identity 74
- Alignment Length 129
- Location of Alignment in SEQ ID NO 1449: from 6 to 131
- Alignment No. 12361
- gi No. 3132829
- % Identity 73.8
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1449: from 6 to 131
- Alignment No. 12362
- gi No. 3776005
- % Identity 72.9
- Alignment Length 156
- Location of Alignment in SEQ ID NO 1449: from 1 to 131
- Alignment No. 12363
- gi No. 3805815
- % Identity 73.2
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1449: from 6 to 131
- Alignment No. 12364
- gi No. 4235116
- % Identity 74
- Alignment Length 129
- Location of Alignment in SEQ ID NO 1449: from 6 to 131
- Alignment No. 12365
- gi No. 4758112
- % Identity 73.2
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1449: from 6 to 131
- Alignment No. 12366
- gi No. 5031659
- % Identity 70.6
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1449: from 6 to 131
- Alignment No. 12367
- gi No. 539961
- % Identity 74
- Alignment Length 129
- Location of Alignment in SEQ ID NO 1449: from 6 to 131

Maximum Length Sequence corresponding to clone ID 259555

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1450

- Ceres seq_id 1500313
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1451
 - Ceres seq_id 1500314
 - Location of start within SEQ ID NO 1450: at 481 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 12368
 - gi No. 1708463
 - % Identity 77.8
 - Alignment Length 262
 - Location of Alignment in SEQ ID NO 1451: from 1 to 203

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1452
 - Ceres seq_id 1500315
 - Location of start within SEQ ID NO 1450: at 514 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 12369
 - gi No. 1708463
 - % Identity 77.8
 - Alignment Length 262
 - Location of Alignment in SEQ ID NO 1452: from 1 to 192

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1453
 - Ceres seq_id 1500316
 - Location of start within SEQ ID NO 1450: at 622 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 12370
 - gi No. 1708463
 - % Identity 77.8
 - Alignment Length 262
 - Location of Alignment in SEQ ID NO 1453: from 1 to 156

Maximum Length Sequence corresponding to clone ID 259571

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1454
 - Ceres seq_id 1500321
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1455
 - Ceres seq_id 1500322
 - Location of start within SEQ ID NO 1454: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1456
 - Ceres seq_id 1500323
 - Location of start within SEQ ID NO 1454: at 158 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12371
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1456: from 38 to 90 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1457
- Ceres seq_id 1500324
- Location of start within SEQ ID NO 1454: at 245 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12372
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1457: from 9 to 61 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 260361

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1458
- Ceres seq_id 1500367

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1459
- Ceres seq_id 1500368
- Location of start within SEQ ID NO 1458: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12373
- Nuclear transition protein 2
- Location within SEQ ID NO 1459: from 17 to 102 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12374
- gi No. 553165
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1459: from 74 to 86

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1460
- Ceres seq_id 1500369
- Location of start within SEQ ID NO 1458: at 44 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12375
- gi No. 347455
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1460: from 27 to 37

Maximum Length Sequence corresponding to clone ID 260368

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1461
- Ceres seq_id 1500370

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1462
- Ceres seq_id 1500371
- Location of start within SEQ ID NO 1461: at 96 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12376
- Zinc finger, C2H2 type
- Location within SEQ ID NO 1462: from 25 to 47 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12377
- gi No. 1361986
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1462: from 15 to 51

- Alignment No. 12378
- gi No. 1362015
- % Identity 76.7
- Alignment Length 30
- Location of Alignment in SEQ ID NO 1462: from 22 to 51

- Alignment No. 12379
- gi No. 1362017
- % Identity 81.5
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1462: from 25 to 51

- Alignment No. 12380
- gi No. 1362018
- % Identity 72
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1462: from 27 to 51

- Alignment No. 12381
- gi No. 1362020
- % Identity 74.1
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1462: from 25 to 51

- Alignment No. 12382
- gi No. 1871188
- % Identity 74.1
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1462: from 25 to 51

- Alignment No. 12383
- gi No. 790687
- % Identity 74.1
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1462: from 25 to 51

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1463
- Ceres seq_id 1500372
- Location of start within SEQ ID NO 1461: at 347 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1464
- Ceres seq_id 1500373
- Location of start within SEQ ID NO 1461: at 460 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 260388

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1465
- Ceres seq id 1500374

(B) Polypeptide Sequence

- ```
- Pat. Appln. SEQ ID NO 1466
- Ceres seq_id 1500375
- Location of start within SEQ ID NO 1465: at 3 nt.
```

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

#### (D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1467
- Ceres seq\_id 1500376
- Location of start within SEQ ID NO 1465: at 100 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12384
- Ubiquitin family
- Location within SEQ ID NO 1467: from 1 to 38 aa.

#### (D) Related Amino Acid Sequences

- ```
- Alignment No. 12385
- gi No. 100525
- % Identity 71
- Alignment Length 31
- Location of Alignment in SEQ ID NO 1467: from 1 to 31

- Alignment No. 12386
- gi No. 1050930
- % Identity 79.2
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1467: from 1 to 24

- Alignment No. 12387
- gi No. 208891
- % Identity 73.9
- Alignment Length 23
- Location of Alignment in SEQ ID NO 1467: from 1 to 23

- Alignment No. 12388
- gi No. 456779
- % Identity 79.2
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1467: from 1 to 24

- Alignment No. 12389
```

- gi No. 899115
- % Identity 75
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1467: from 1 to 24
- Alignment No. 12390
- gi No. 91870
- % Identity 73.9
- Alignment Length 23
- Location of Alignment in SEQ ID NO 1467: from 1 to 23

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1468
- Ceres seq_id 1500377
- Location of start within SEQ ID NO 1465: at 282 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 260615

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1469
- Ceres seq_id 1500387

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1470
- Ceres seq_id 1500388
- Location of start within SEQ ID NO 1469: at 144 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12391
- Mitochondrial carrier proteins
- Location within SEQ ID NO 1470: from 23 to 223 aa.
- Alignment No. 12392
- Mitochondrial carrier proteins
- Location within SEQ ID NO 1470: from 37 to 322 aa.
- Alignment No. 12393
- Mitochondrial carrier proteins
- Location within SEQ ID NO 1470: from 146 to 327 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1471
- Ceres seq_id 1500389
- Location of start within SEQ ID NO 1469: at 150 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12394
- Mitochondrial carrier proteins
- Location within SEQ ID NO 1471: from 21 to 221 aa.
- Alignment No. 12395
- Mitochondrial carrier proteins
- Location within SEQ ID NO 1471: from 35 to 320 aa.
- Alignment No. 12396

- Mitochondrial carrier proteins
- Location within SEQ ID NO 1471: from 144 to 325 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1472
- Ceres seq_id 1500390
- Location of start within SEQ ID NO 1469: at 342 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12397
- Mitochondrial carrier proteins
- Location within SEQ ID NO 1472: from 1 to 157 aa.
- Alignment No. 12398
- Mitochondrial carrier proteins
- Location within SEQ ID NO 1472: from 1 to 256 aa.
- Alignment No. 12399
- Mitochondrial carrier proteins
- Location within SEQ ID NO 1472: from 80 to 261 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 260891

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1473
- Ceres seq_id 1500391

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1474
- Ceres seq_id 1500392
- Location of start within SEQ ID NO 1473: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12400
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 1474: from 5 to 108 aa.
- Alignment No. 12401
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 1474: from 10 to 108 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1475
- Ceres seq_id 1500393
- Location of start within SEQ ID NO 1473: at 27 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12402
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 1475: from 1 to 100 aa.
- Alignment No. 12403
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 1475: from 2 to 100 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1476
- Ceres seq_id 1500394
- Location of start within SEQ ID NO 1473: at 120 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12404
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 1476: from 1 to 69 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 260925

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1477
- Ceres seq_id 1500395

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1478
- Ceres seq_id 1500396
- Location of start within SEQ ID NO 1477: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1479
- Ceres seq_id 1500397
- Location of start within SEQ ID NO 1477: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12405
- Sperm histone P2
- Location within SEQ ID NO 1479: from 15 to 73 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1480
- Ceres seq_id 1500398
- Location of start within SEQ ID NO 1477: at 68 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 261148

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1481
- Ceres seq_id 1500407

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1482
- Ceres seq_id 1500408
- Location of start within SEQ ID NO 1481: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1483
- Ceres seq_id 1500409
- Location of start within SEQ ID NO 1481: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12406
- GTP cyclohydrolase I
- Location within SEQ ID NO 1483: from 80 to 131 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1484
- Ceres seq_id 1500410
- Location of start within SEQ ID NO 1481: at 128 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12407
- GTP cyclohydrolase I
- Location within SEQ ID NO 1484: from 38 to 89 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 261372

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1485
- Ceres seq_id 1500422

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1486
- Ceres seq_id 1500423
- Location of start within SEQ ID NO 1485: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12408
- Ribosomal protein L21e
- Location within SEQ ID NO 1486: from 28 to 108 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12409
- gi No. 2851508
- % Identity 87.8
- Alignment Length 82
- Location of Alignment in SEQ ID NO 1486: from 27 to 108

- Alignment No. 12410

- gi No. 3885884

- % Identity 92.7

- Alignment Length 82

- Location of Alignment in SEQ ID NO 1486: from 27 to 108

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1487
- Ceres seq_id 1500424

- Location of start within SEQ ID NO 1485: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1488
- Ceres seq_id 1500425
- Location of start within SEQ ID NO 1485: at 80 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12411
- Ribosomal protein L21e
- Location within SEQ ID NO 1488: from 2 to 82 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12412
- gi No. 2851508
- % Identity 87.8
- Alignment Length 82
- Location of Alignment in SEQ ID NO 1488: from 1 to 82
- Alignment No. 12413
- gi No. 3885884
- % Identity 92.7
- Alignment Length 82
- Location of Alignment in SEQ ID NO 1488: from 1 to 82

Maximum Length Sequence corresponding to clone ID 261674

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1489
- Ceres seq_id 1500464

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1490
- Ceres seq_id 1500465
- Location of start within SEQ ID NO 1489: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12414
- gi No. 2145062
- % Identity 90.9
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1490: from 82 to 92

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1491
- Ceres seq_id 1500466
- Location of start within SEQ ID NO 1489: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12415
- Collagen triple helix repeat (20 copies)
- Location within SEQ ID NO 1491: from 11 to 59 aa.

(D) Related Amino Acid Sequences

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(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1492
- Ceres seq_id 1500467
- Location of start within SEQ ID NO 1489: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12416
- gi No. 3875441
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1492: from 81 to 97

Maximum Length Sequence corresponding to clone ID 261748

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1493
- Ceres seq_id 1500468

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1494
- Ceres seq_id 1500469
- Location of start within SEQ ID NO 1493: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12417
- Sm protein
- Location within SEQ ID NO 1494: from 94 to 155 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1495
- Ceres seq_id 1500470
- Location of start within SEQ ID NO 1493: at 179 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12418
- Sm protein
- Location within SEQ ID NO 1495: from 35 to 96 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 261790

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1496
- Ceres seq_id 1500474

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1497
- Ceres seq_id 1500475
- Location of start within SEQ ID NO 1496: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1498
- Ceres seq_id 1500476
- Location of start within SEQ ID NO 1496: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12419
- Cytochrome P450
- Location within SEQ ID NO 1498: from 59 to 127 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1499
- Ceres seq_id 1500477
- Location of start within SEQ ID NO 1496: at 72 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12420
- Cytochrome P450
- Location within SEQ ID NO 1499: from 36 to 104 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 261801

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1500
- Ceres seq_id 1500478

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1501
- Ceres seq_id 1500479
- Location of start within SEQ ID NO 1500: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12421
- Collagen triple helix repeat (20 copies)
- Location within SEQ ID NO 1501: from 49 to 108 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1502
- Ceres seq_id 1500480
- Location of start within SEQ ID NO 1500: at 161 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 261825

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1503
- Ceres seq_id 1500481

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1504
- Ceres seq_id 1500482
- Location of start within SEQ ID NO 1503: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12422
- Metallo-beta-lactamase superfamily

- Location within SEQ ID NO 1504: from 56 to 160 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1505
- Ceres seq_id 1500483
- Location of start within SEQ ID NO 1503: at 68 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12423
- Metallo-beta-lactamase superfamily
- Location within SEQ ID NO 1505: from 34 to 138 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 261831

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1506
- Ceres seq_id 1500487

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1507
- Ceres seq_id 1500488
- Location of start within SEQ ID NO 1506: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1508
- Ceres seq_id 1500489
- Location of start within SEQ ID NO 1506: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12424
- gi No. 132933
- % Identity 77.8
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1508: from 26 to 52

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1509
- Ceres seq_id 1500490
- Location of start within SEQ ID NO 1506: at 221 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 261853

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1510
- Ceres seq_id 1500491

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1511
- Ceres seq_id 1500492
- Location of start within SEQ ID NO 1510: at 201 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12425
- gi No. 3834316
- % Identity 96.9
- Alignment Length 224
- Location of Alignment in SEQ ID NO 1511: from 1 to 173

Maximum Length Sequence corresponding to clone ID 261966

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1512
- Ceres seq_id 1500495

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1513
- Ceres seq_id 1500496
- Location of start within SEQ ID NO 1512: at 78 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12426
- gi No. 131176
- % Identity 71.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1513: from 1 to 135

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1514
- Ceres seq_id 1500497
- Location of start within SEQ ID NO 1512: at 93 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12427
- gi No. 131176
- % Identity 71.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1514: from 1 to 130

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1515
- Ceres seq_id 1500498
- Location of start within SEQ ID NO 1512: at 117 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12428
- gi No. 131176
- % Identity 71.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1515: from 1 to 122

Maximum Length Sequence corresponding to clone ID 261978

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1516
- Ceres seq_id 1500501

(B) Polypeptide Sequence

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- Pat. Appln. SEQ ID NO 1517
- Ceres seq_id 1500502
- Location of start within SEQ ID NO 1516: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12429
- gi No. 1321924
- % Identity 73.9
- Alignment Length 23
- Location of Alignment in SEQ ID NO 1517: from 100 to 122

- Alignment No. 12430
- gi No. 1944132
- % Identity 81.8
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1517: from 101 to 122

- Alignment No. 12431
- gi No. 2894607
- % Identity 72
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1517: from 101 to 125

- Alignment No. 12432
- gi No. 4218537
- % Identity 74.1
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1517: from 96 to 122

- Alignment No. 12433
- gi No. 5091624
- % Identity 80
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1517: from 103 to 122

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1518
- Ceres seq_id 1500503
- Location of start within SEQ ID NO 1516: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 261997

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1519
- Ceres seq_id 1500504

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1520
- Ceres seq_id 1500505
- Location of start within SEQ ID NO 1519: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12434
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1520: from 64 to 161 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12435
- gi No. 1168470
- % Identity 72.4
- Alignment Length 134
- Location of Alignment in SEQ ID NO 1520: from 28 to 161

- Alignment No. 12436
- gi No. 1168471
- % Identity 83.3
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1520: from 138 to 161

- Alignment No. 12437
- gi No. 4432889
- % Identity 83.3
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1520: from 138 to 161

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1521
- Ceres seq_id 1500506
- Location of start within SEQ ID NO 1519: at 44 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12438
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1521: from 50 to 147 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12439
- gi No. 1168470
- % Identity 72.4
- Alignment Length 134
- Location of Alignment in SEQ ID NO 1521: from 14 to 147

- Alignment No. 12440
- gi No. 1168471
- % Identity 83.3
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1521: from 124 to 147

- Alignment No. 12441
- gi No. 4432889
- % Identity 83.3
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1521: from 124 to 147

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1522
- Ceres seq_id 1500507
- Location of start within SEQ ID NO 1519: at 173 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12442
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1522: from 7 to 104 aa.

(D) Related Amino Acid Sequences

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- Alignment No. 12443
- gi No. 1168470
- % Identity 72.4
- Alignment Length 134
- Location of Alignment in SEQ ID NO 1522: from 1 to 104

- Alignment No. 12444
- gi No. 1168471
- % Identity 83.3
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1522: from 81 to 104

- Alignment No. 12445
- gi No. 4432889
- % Identity 83.3
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1522: from 81 to 104

Maximum Length Sequence corresponding to clone ID 262057

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1523
- Ceres seq_id 1500516

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1524
- Ceres seq_id 1500517
- Location of start within SEQ ID NO 1523: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1525
- Ceres seq_id 1500518
- Location of start within SEQ ID NO 1523: at 303 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12446
- gi No. 4966357
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1525: from 32 to 52

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1526
- Ceres seq_id 1500519
- Location of start within SEQ ID NO 1523: at 346 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 262215

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1527
- Ceres seq_id 1500539

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1528
- Ceres seq_id 1500540

- Location of start within SEQ ID NO 1527: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12447
- gi No. 2342684
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 1528: from 1 to 16
- Alignment No. 12448
- gi No. 3540195
- % Identity 75
- Alignment Length 28
- Location of Alignment in SEQ ID NO 1528: from 3 to 30

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1529
- Ceres seq_id 1500541
- Location of start within SEQ ID NO 1527: at 99 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1530
- Ceres seq_id 1500542
- Location of start within SEQ ID NO 1527: at 114 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 262351

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1531
- Ceres seq_id 1500554

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1532
- Ceres seq_id 1500555
- Location of start within SEQ ID NO 1531: at 189 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12449
- gi No. 4468993
- % Identity 99.7
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1532: from 1 to 363
- Alignment No. 12450
- gi No. 4539337
- % Identity 92.2
- Alignment Length 51
- Location of Alignment in SEQ ID NO 1532: from 313 to 363
- Alignment No. 12451
- gi No. 4539340

- % Identity 98.1
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1532: from 1 to 363
- Alignment No. 12452
- gi No. 4895222
- % Identity 98.6
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1532: from 293 to 363

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1533
- Ceres seq_id 1500556
- Location of start within SEQ ID NO 1531: at 246 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12453
- gi No. 4468993
- % Identity 99.7
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1533: from 1 to 344
- Alignment No. 12454
- gi No. 4539337
- % Identity 92.2
- Alignment Length 51
- Location of Alignment in SEQ ID NO 1533: from 294 to 344
- Alignment No. 12455
- gi No. 4539340
- % Identity 98.1
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1533: from 1 to 344
- Alignment No. 12456
- gi No. 4895222
- % Identity 98.6
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1533: from 274 to 344

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1534
- Ceres seq_id 1500557
- Location of start within SEQ ID NO 1531: at 585 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12457
- gi No. 4468993
- % Identity 99.7
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1534: from 1 to 231
- Alignment No. 12458
- gi No. 4539337
- % Identity 92.2
- Alignment Length 51
- Location of Alignment in SEQ ID NO 1534: from 181 to 231

- Alignment No. 12459
- gi No. 4539340
- % Identity 98.1
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1534: from 1 to 231

- Alignment No. 12460
- gi No. 4895222
- % Identity 98.6
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1534: from 161 to 231

Maximum Length Sequence corresponding to clone ID 262550

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1535
- Ceres seq_id 1500558

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1536
- Ceres seq_id 1500559
- Location of start within SEQ ID NO 1535: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12461
- gi No. 4982480
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1536: from 123 to 178

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1537
- Ceres seq_id 1500560
- Location of start within SEQ ID NO 1535: at 14 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12462
- gi No. 4982480
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1537: from 119 to 174

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1538
- Ceres seq_id 1500561
- Location of start within SEQ ID NO 1535: at 104 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12463
- gi No. 4982480
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1538: from 89 to 144

Maximum Length Sequence corresponding to clone ID 262802

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1539
- Ceres seq_id 1500562

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1540
- Ceres seq_id 1500563
- Location of start within SEQ ID NO 1539: at 843 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12464
- Cytochrome P450
- Location within SEQ ID NO 1540: from 1 to 226 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1541
- Ceres seq_id 1500564
- Location of start within SEQ ID NO 1539: at 960 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12465
- Cytochrome P450
- Location within SEQ ID NO 1541: from 1 to 187 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1542
- Ceres seq_id 1500565
- Location of start within SEQ ID NO 1539: at 1095 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12466
- Cytochrome P450
- Location within SEQ ID NO 1542: from 1 to 142 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 263816

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1543
- Ceres seq_id 1500614

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1544
- Ceres seq_id 1500615
- Location of start within SEQ ID NO 1543: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12467
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1544: from 51 to 308 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12468
- gi No. 3450842
- % Identity 76.9
- Alignment Length 277

- Location of Alignment in SEQ ID NO 1544: from 37 to 313

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1545
- Ceres seq_id 1500616
- Location of start within SEQ ID NO 1543: at 84 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12469
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1545: from 24 to 281 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12470
- gi No. 3450842
- % Identity 76.9
- Alignment Length 277
- Location of Alignment in SEQ ID NO 1545: from 10 to 286

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1546
- Ceres seq_id 1500617
- Location of start within SEQ ID NO 1543: at 339 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12471
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1546: from 1 to 196 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12472
- gi No. 3450842
- % Identity 76.9
- Alignment Length 277
- Location of Alignment in SEQ ID NO 1546: from 1 to 201

Maximum Length Sequence corresponding to clone ID 264799

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1547
- Ceres seq_id 1500618

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1548
- Ceres seq_id 1500619
- Location of start within SEQ ID NO 1547: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12473
- Jacalin-like lectin domain
- Location within SEQ ID NO 1548: from 107 to 244 aa.
- Alignment No. 12474
- Jacalin-like lectin domain
- Location within SEQ ID NO 1548: from 264 to 391 aa.
- Alignment No. 12475
- von Willebrand factor type A domain
- Location within SEQ ID NO 1548: from 104 to 212 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12476
- gi No. 3402674
- % Identity 99.4
- Alignment Length 311
- Location of Alignment in SEQ ID NO 1548: from 92 to 402

- Alignment No. 12477
- gi No. 3402676
- % Identity 78.3
- Alignment Length 315
- Location of Alignment in SEQ ID NO 1548: from 92 to 404

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1549
- Ceres seq_id 1500620
- Location of start within SEQ ID NO 1547: at 133 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12478
- Jacalin-like lectin domain
- Location within SEQ ID NO 1549: from 63 to 200 aa.

- Alignment No. 12479
- Jacalin-like lectin domain
- Location within SEQ ID NO 1549: from 220 to 347 aa.

- Alignment No. 12480
- von Willebrand factor type A domain
- Location within SEQ ID NO 1549: from 60 to 168 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12481
- gi No. 3402674
- % Identity 99.4
- Alignment Length 311
- Location of Alignment in SEQ ID NO 1549: from 48 to 358

- Alignment No. 12482
- gi No. 3402676
- % Identity 78.3
- Alignment Length 315
- Location of Alignment in SEQ ID NO 1549: from 48 to 360

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1550
- Ceres seq_id 1500621
- Location of start within SEQ ID NO 1547: at 274 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12483
- Jacalin-like lectin domain
- Location within SEQ ID NO 1550: from 16 to 153 aa.

- Alignment No. 12484
- Jacalin-like lectin domain
- Location within SEQ ID NO 1550: from 173 to 300 aa.

- Alignment No. 12485

- von Willebrand factor type A domain
- Location within SEQ ID NO 1550: from 13 to 121 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12486
 - gi No. 3402674
 - % Identity 99.4
 - Alignment Length 311
 - Location of Alignment in SEQ ID NO 1550: from 1 to 311
-
- Alignment No. 12487
 - gi No. 3402676
 - % Identity 78.3
 - Alignment Length 315
 - Location of Alignment in SEQ ID NO 1550: from 1 to 313

Maximum Length Sequence corresponding to clone ID 264837

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1551
- Ceres seq_id 1500622

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1552
- Ceres seq_id 1500623
- Location of start within SEQ ID NO 1551: at 23 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12488
 - gi No. 4586265
 - % Identity 70.6
 - Alignment Length 143
 - Location of Alignment in SEQ ID NO 1552: from 1 to 136
-
- Alignment No. 12489
 - gi No. 5123937
 - % Identity 100
 - Alignment Length 136
 - Location of Alignment in SEQ ID NO 1552: from 1 to 136

Maximum Length Sequence corresponding to clone ID 265926

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1553
- Ceres seq_id 1500633

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1554
- Ceres seq_id 1500634
- Location of start within SEQ ID NO 1553: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12490
 - gi No. 1171429
 - % Identity 80
 - Alignment Length 30
 - Location of Alignment in SEQ ID NO 1554: from 7 to 36
-
- Alignment No. 12491
 - gi No. 2129537
 - % Identity 80

- ```
- Alignment Length 30
- Location of Alignment in SEQ ID NO 1554: from 7 to 36

- Alignment No. 12492
- gi No. 2652938
- % Identity 80.6
- Alignment Length 31
- Location of Alignment in SEQ ID NO 1554: from 6 to 36

- Alignment No. 12493
- gi No. 4836931
- % Identity 77.4
- Alignment Length 31
- Location of Alignment in SEQ ID NO 1554: from 6 to 36
```

Maximum Length Sequence corresponding to clone ID 266518

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1555
- Ceres seq id 1500645

(B) Polypeptide Sequence

- ```
- Pat. Appln. SEQ ID NO 1556
- Ceres seq_id 1500646
- Location of start within SEQ ID NO 1555: at 84 nt.
```

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12494
- short chain dehydrogenase
- Location within SEQ ID NO 1556: from 72 to 264 aa.

(D) Related Amino Acid Sequences

- ```

- Alignment No. 12495
- gi No. 348718
- % Identity 72.2
- Alignment Length 306
- Location of Alignment in SEQ ID NO 1556: from 50 to 353

- Alignment No. 12496
- gi No. 348720
- % Identity 71.1
- Alignment Length 329
- Location of Alignment in SEQ ID NO 1556: from 50 to 376

- Alignment No. 12497
- gi No. 4469027
- % Identity 100
- Alignment Length 232
- Location of Alignment in SEQ ID NO 1556: from 1 to 232

- Alignment No. 12498
- gi No. 4972108
- % Identity 100
- Alignment Length 176
- Location of Alignment in SEQ ID NO 1556: from 201 to 376

- Alignment No. 12499
- gi No. 957251
- % Identity 100
- Alignment Length 305
- Location of Alignment in SEQ ID NO 1556: from 72 to 376

```

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1557
- Ceres seq\_id 1500647
- Location of start within SEQ ID NO 1555: at 150 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12500
- short chain dehydrogenase
- Location within SEQ ID NO 1557: from 50 to 242 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12501
- gi No. 348718
- % Identity 72.2
- Alignment Length 306
- Location of Alignment in SEQ ID NO 1557: from 28 to 331
  
- Alignment No. 12502
- gi No. 348720
- % Identity 71.1
- Alignment Length 329
- Location of Alignment in SEQ ID NO 1557: from 28 to 354
  
- Alignment No. 12503
- gi No. 4469027
- % Identity 100
- Alignment Length 232
- Location of Alignment in SEQ ID NO 1557: from 1 to 210
  
- Alignment No. 12504
- gi No. 4972108
- % Identity 100
- Alignment Length 176
- Location of Alignment in SEQ ID NO 1557: from 179 to 354
  
- Alignment No. 12505
- gi No. 957251
- % Identity 100
- Alignment Length 305
- Location of Alignment in SEQ ID NO 1557: from 50 to 354

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1558
- Ceres seq\_id 1500648
- Location of start within SEQ ID NO 1555: at 159 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12506
- short chain dehydrogenase
- Location within SEQ ID NO 1558: from 47 to 239 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12507
- gi No. 348718
- % Identity 72.2
- Alignment Length 306
- Location of Alignment in SEQ ID NO 1558: from 25 to 328
  
- Alignment No. 12508

- gi No. 348720
- % Identity 71.1
- Alignment Length 329
- Location of Alignment in SEQ ID NO 1558: from 25 to 351
  
- Alignment No. 12509
- gi No. 4469027
- % Identity 100
- Alignment Length 232
- Location of Alignment in SEQ ID NO 1558: from 1 to 207
  
- Alignment No. 12510
- gi No. 4972108
- % Identity 100
- Alignment Length 176
- Location of Alignment in SEQ ID NO 1558: from 176 to 351
  
- Alignment No. 12511
- gi No. 957251
- % Identity 100
- Alignment Length 305
- Location of Alignment in SEQ ID NO 1558: from 47 to 351

Maximum Length Sequence corresponding to clone ID 266520

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1559
- Ceres seq\_id 1500649

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1560
- Ceres seq\_id 1500650
- Location of start within SEQ ID NO 1559: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12512
- gi No. 3426051
- % Identity 94.4
- Alignment Length 319
- Location of Alignment in SEQ ID NO 1560: from 14 to 332

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1561
- Ceres seq\_id 1500651
- Location of start within SEQ ID NO 1559: at 258 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12513
- gi No. 3426051
- % Identity 94.4
- Alignment Length 319
- Location of Alignment in SEQ ID NO 1561: from 1 to 247

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1562
- Ceres seq\_id 1500652
- Location of start within SEQ ID NO 1559: at 267 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12514
- gi No. 3426051
- % Identity 94.4
- Alignment Length 319
- Location of Alignment in SEQ ID NO 1562: from 1 to 244

Maximum Length Sequence corresponding to clone ID 266544

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1563
- Ceres seq\_id 1500653

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1564
- Ceres seq\_id 1500654
- Location of start within SEQ ID NO 1563: at 118 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12515
- Regulator of chromosome condensation (RCC1)
- Location within SEQ ID NO 1564: from 34 to 92 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1565
- Ceres seq\_id 1500655
- Location of start within SEQ ID NO 1563: at 218 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1566
- Ceres seq\_id 1500656
- Location of start within SEQ ID NO 1563: at 247 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12516
- Regulator of chromosome condensation (RCC1)
- Location within SEQ ID NO 1566: from 1 to 49 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 266710

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1567
- Ceres seq\_id 1500661

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1568
- Ceres seq\_id 1500662
- Location of start within SEQ ID NO 1567: at 27 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12517

- gi No. 2980782
- % Identity 84.3
- Alignment Length 168
- Location of Alignment in SEQ ID NO 1568: from 1 to 157

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1569
- Ceres seq\_id 1500663
- Location of start within SEQ ID NO 1567: at 33 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12518
- gi No. 2980782
- % Identity 84.3
- Alignment Length 168
- Location of Alignment in SEQ ID NO 1569: from 1 to 155

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1570
- Ceres seq\_id 1500664
- Location of start within SEQ ID NO 1567: at 36 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12519
- gi No. 2980782
- % Identity 84.3
- Alignment Length 168
- Location of Alignment in SEQ ID NO 1570: from 1 to 154

Maximum Length Sequence corresponding to clone ID 266712

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1571
- Ceres seq\_id 1500665

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1572
- Ceres seq\_id 1500666
- Location of start within SEQ ID NO 1571: at 48 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12520
- RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- Location within SEQ ID NO 1572: from 8 to 79 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12521
- gi No. 1076672
- % Identity 71.6
- Alignment Length 102
- Location of Alignment in SEQ ID NO 1572: from 1 to 100
- Alignment No. 12522
- gi No. 1076731
- % Identity 73.8
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1572: from 1 to 100

- Alignment No. 12523
- gi No. 1076731
- % Identity 72.4
- Alignment Length 105
- Location of Alignment in SEQ ID NO 1572: from 1 to 101
  
- Alignment No. 12524
- gi No. 1229138
- % Identity 72.3
- Alignment Length 101
- Location of Alignment in SEQ ID NO 1572: from 1 to 101
  
- Alignment No. 12525
- gi No. 1346180
- % Identity 78.4
- Alignment Length 97
- Location of Alignment in SEQ ID NO 1572: from 3 to 99
  
- Alignment No. 12526
- gi No. 1346181
- % Identity 76.3
- Alignment Length 97
- Location of Alignment in SEQ ID NO 1572: from 3 to 99
  
- Alignment No. 12527
- gi No. 1710625
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1572: from 86 to 99
  
- Alignment No. 12528
- gi No. 1710626
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1572: from 86 to 96
  
- Alignment No. 12529
- gi No. 1710626
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1572: from 86 to 99
  
- Alignment No. 12530
- gi No. 1710626
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1572: from 86 to 100
  
- Alignment No. 12531
- gi No. 1710627
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1572: from 88 to 100
  
- Alignment No. 12532
- gi No. 1934994
- % Identity 73.7
- Alignment Length 99
- Location of Alignment in SEQ ID NO 1572: from 2 to 100
  
- Alignment No. 12533

- gi No. 2119042
- % Identity 77.9
- Alignment Length 104
- Location of Alignment in SEQ ID NO 1572: from 1 to 101
  
- Alignment No. 12534
- gi No. 2119042
- % Identity 71.9
- Alignment Length 114
- Location of Alignment in SEQ ID NO 1572: from 1 to 101
  
- Alignment No. 12535
- gi No. 2119043
- % Identity 74.3
- Alignment Length 101
- Location of Alignment in SEQ ID NO 1572: from 1 to 101
  
- Alignment No. 12536
- gi No. 2119044
- % Identity 75.7
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1572: from 1 to 100
  
- Alignment No. 12537
- gi No. 2129944
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1572: from 88 to 100
  
- Alignment No. 12538
- gi No. 2143460
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1572: from 87 to 98
  
- Alignment No. 12539
- gi No. 2226370
- % Identity 76.2
- Alignment Length 105
- Location of Alignment in SEQ ID NO 1572: from 1 to 101
  
- Alignment No. 12540
- gi No. 2267567
- % Identity 73.3
- Alignment Length 101
- Location of Alignment in SEQ ID NO 1572: from 2 to 101
  
- Alignment No. 12541
- gi No. 2267593
- % Identity 70.6
- Alignment Length 102
- Location of Alignment in SEQ ID NO 1572: from 3 to 101
  
- Alignment No. 12542
- gi No. 2293480
- % Identity 71.6
- Alignment Length 102
- Location of Alignment in SEQ ID NO 1572: from 3 to 101
  
- Alignment No. 12543
- gi No. 2293480



- % Identity 70.4
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1572: from 3 to 100
  
- Alignment No. 12544
- gi No. 2331131
- % Identity 72.7
- Alignment Length 99
- Location of Alignment in SEQ ID NO 1572: from 3 to 101
  
- Alignment No. 12545
- gi No. 2331133
- % Identity 71.6
- Alignment Length 102
- Location of Alignment in SEQ ID NO 1572: from 3 to 101
  
- Alignment No. 12546
- gi No. 2624326
- % Identity 74.5
- Alignment Length 102
- Location of Alignment in SEQ ID NO 1572: from 3 to 101
  
- Alignment No. 12547
- gi No. 2668742
- % Identity 71.2
- Alignment Length 104
- Location of Alignment in SEQ ID NO 1572: from 2 to 101
  
- Alignment No. 12548
- gi No. 2674201
- % Identity 71.2
- Alignment Length 104
- Location of Alignment in SEQ ID NO 1572: from 2 to 101
  
- Alignment No. 12549
- gi No. 283664
- % Identity 70.6
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1572: from 84 to 100
  
- Alignment No. 12550
- gi No. 3914466
- % Identity 85
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1572: from 59 to 78
  
- Alignment No. 12551
- gi No. 423560
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1572: from 87 to 98
  
- Alignment No. 12552
- gi No. 4567236
- % Identity 82.5
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1572: from 39 to 101
  
- Alignment No. 12553
- gi No. 4567236
- % Identity 73.2

- Alignment Length 71
- Location of Alignment in SEQ ID NO 1572: from 39 to 101
  
- Alignment No. 12554
- gi No. 4587684
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1572: from 49 to 65
  
- Alignment No. 12555
- gi No. 469072
- % Identity 76.2
- Alignment Length 101
- Location of Alignment in SEQ ID NO 1572: from 1 to 101
  
- Alignment No. 12556
- gi No. 4938296
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1572: from 86 to 100
  
- Alignment No. 12557
- gi No. 4938296
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1572: from 86 to 100
  
- Alignment No. 12558
- gi No. 5031693
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1572: from 88 to 100
  
- Alignment No. 12559
- gi No. 542649
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1572: from 86 to 99
  
- Alignment No. 12560
- gi No. 544416
- % Identity 84
- Alignment Length 100
- Location of Alignment in SEQ ID NO 1572: from 1 to 100
  
- Alignment No. 12561
- gi No. 544416
- % Identity 76.1
- Alignment Length 113
- Location of Alignment in SEQ ID NO 1572: from 1 to 101
  
- Alignment No. 12562
- gi No. 544421
- % Identity 70.4
- Alignment Length 81
- Location of Alignment in SEQ ID NO 1572: from 22 to 100
  
- Alignment No. 12563
- gi No. 544423
- % Identity 74
- Alignment Length 100

- Location of Alignment in SEQ ID NO 1572: from 2 to 101
- Alignment No. 12564
- gi No. 544424
- % Identity 79.8
- Alignment Length 99
- Location of Alignment in SEQ ID NO 1572: from 3 to 101
- Alignment No. 12565
- gi No. 544424
- % Identity 73.8
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1572: from 3 to 101
- Alignment No. 12566
- gi No. 544425
- % Identity 92.9
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1572: from 88 to 101
- Alignment No. 12567
- gi No. 544425
- % Identity 94.1
- Alignment Length 101
- Location of Alignment in SEQ ID NO 1572: from 1 to 101
- Alignment No. 12568
- gi No. 544425
- % Identity 82.9
- Alignment Length 117
- Location of Alignment in SEQ ID NO 1572: from 1 to 101
- Alignment No. 12569
- gi No. 544426
- % Identity 82.2
- Alignment Length 101
- Location of Alignment in SEQ ID NO 1572: from 1 to 101
- Alignment No. 12570
- gi No. 544426
- % Identity 79.2
- Alignment Length 106
- Location of Alignment in SEQ ID NO 1572: from 1 to 99
- Alignment No. 12571
- gi No. 5726567
- % Identity 70
- Alignment Length 100
- Location of Alignment in SEQ ID NO 1572: from 2 to 101
- Alignment No. 12572
- gi No. 82696
- % Identity 71
- Alignment Length 100
- Location of Alignment in SEQ ID NO 1572: from 2 to 100
- Alignment No. 12573
- gi No. 974605
- % Identity 74.3
- Alignment Length 101
- Location of Alignment in SEQ ID NO 1572: from 1 to 101

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- Alignment No. 12574
- gi No. 974605
- % Identity 73.3
- Alignment Length 105
- Location of Alignment in SEQ ID NO 1572: from 1 to 100

Maximum Length Sequence corresponding to clone ID 266730

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1573
- Ceres seq\_id 1500667

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1574
- Ceres seq\_id 1500668
- Location of start within SEQ ID NO 1573: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1575
- Ceres seq\_id 1500669
- Location of start within SEQ ID NO 1573: at 90 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1576
- Ceres seq\_id 1500670
- Location of start within SEQ ID NO 1573: at 277 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12575
- gi No. 1513292
- % Identity 71.4
- Alignment Length 42
- Location of Alignment in SEQ ID NO 1576: from 9 to 49

- Alignment No. 12576

- gi No. 4539026

- % Identity 70.3

- Alignment Length 37

- Location of Alignment in SEQ ID NO 1576: from 12 to 45

Maximum Length Sequence corresponding to clone ID 266771

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1577
- Ceres seq\_id 1500675

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1578
- Ceres seq\_id 1500676
- Location of start within SEQ ID NO 1577: at 450 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12577

- Zinc finger, C2H2 type
- Location within SEQ ID NO 1578: from 57 to 79 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12578
- gi No. 3551247
- % Identity 93
- Alignment Length 200
- Location of Alignment in SEQ ID NO 1578: from 3 to 202

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1579
- Ceres seq\_id 1500677
- Location of start within SEQ ID NO 1577: at 645 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12579
- gi No. 3551247
- % Identity 93
- Alignment Length 200
- Location of Alignment in SEQ ID NO 1579: from 1 to 137

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1580
- Ceres seq\_id 1500678
- Location of start within SEQ ID NO 1577: at 675 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12580
- gi No. 3551247
- % Identity 93
- Alignment Length 200
- Location of Alignment in SEQ ID NO 1580: from 1 to 127

Maximum Length Sequence corresponding to clone ID 266884

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1581
- Ceres seq\_id 1500679

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1582
- Ceres seq\_id 1500680
- Location of start within SEQ ID NO 1581: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12581
- Helix-loop-helix DNA-binding domain
- Location within SEQ ID NO 1582: from 69 to 114 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12582
- gi No. 4914417
- % Identity 72.2
- Alignment Length 116
- Location of Alignment in SEQ ID NO 1582: from 15 to 129

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1583
- Ceres seq\_id 1500681
- Location of start within SEQ ID NO 1581: at 44 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12583
- Helix-loop-helix DNA-binding domain
- Location within SEQ ID NO 1583: from 55 to 100 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12584
- gi No. 4914417
- % Identity 72.2
- Alignment Length 116
- Location of Alignment in SEQ ID NO 1583: from 1 to 115

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1584
- Ceres seq\_id 1500682
- Location of start within SEQ ID NO 1581: at 345 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 266907

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1585
- Ceres seq\_id 1500683

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1586
- Ceres seq\_id 1500684
- Location of start within SEQ ID NO 1585: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12585
- gi No. 5080769
- % Identity 100
- Alignment Length 155
- Location of Alignment in SEQ ID NO 1586: from 17 to 171

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1587
- Ceres seq\_id 1500685
- Location of start within SEQ ID NO 1585: at 49 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12586
- gi No. 5080769
- % Identity 100
- Alignment Length 155
- Location of Alignment in SEQ ID NO 1587: from 1 to 155

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1588
- Ceres seq\_id 1500686

- Location of start within SEQ ID NO 1585: at 169 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12587
- gi No. 5080769
- % Identity 100
- Alignment Length 155
- Location of Alignment in SEQ ID NO 1588: from 1 to 115

Maximum Length Sequence corresponding to clone ID 267121

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1589
- Ceres seq\_id 1500687

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1590
- Ceres seq\_id 1500688
- Location of start within SEQ ID NO 1589: at 149 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12588
- Myb-like DNA-binding domain
- Location within SEQ ID NO 1590: from 5 to 51 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12589
- gi No. 2832480
- % Identity 100
- Alignment Length 45
- Location of Alignment in SEQ ID NO 1590: from 45 to 89
  
- Alignment No. 12590
- gi No. 2832554
- % Identity 73.3
- Alignment Length 45
- Location of Alignment in SEQ ID NO 1590: from 45 to 89
  
- Alignment No. 12591
- gi No. 3063725
- % Identity 93.3
- Alignment Length 45
- Location of Alignment in SEQ ID NO 1590: from 45 to 89
  
- Alignment No. 12592
- gi No. 3941468
- % Identity 98.4
- Alignment Length 249
- Location of Alignment in SEQ ID NO 1590: from 1 to 249
  
- Alignment No. 12593
- gi No. 3941496
- % Identity 81.4
- Alignment Length 43
- Location of Alignment in SEQ ID NO 1590: from 66 to 108
  
- Alignment No. 12594
- gi No. 4490312
- % Identity 77.1
- Alignment Length 109

- Location of Alignment in SEQ ID NO 1590: from 1 to 108

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1591
- Ceres seq\_id 1500689
- Location of start within SEQ ID NO 1589: at 152 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12595
- Myb-like DNA-binding domain
- Location within SEQ ID NO 1591: from 4 to 50 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12596
- gi No. 2832480
- % Identity 100
- Alignment Length 45
- Location of Alignment in SEQ ID NO 1591: from 44 to 88
- Alignment No. 12597
- gi No. 2832554
- % Identity 73.3
- Alignment Length 45
- Location of Alignment in SEQ ID NO 1591: from 44 to 88
- Alignment No. 12598
- gi No. 3063725
- % Identity 93.3
- Alignment Length 45
- Location of Alignment in SEQ ID NO 1591: from 44 to 88
- Alignment No. 12599
- gi No. 3941468
- % Identity 98.4
- Alignment Length 249
- Location of Alignment in SEQ ID NO 1591: from 1 to 248
- Alignment No. 12600
- gi No. 3941496
- % Identity 81.4
- Alignment Length 43
- Location of Alignment in SEQ ID NO 1591: from 65 to 107
- Alignment No. 12601
- gi No. 4490312
- % Identity 77.1
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1591: from 1 to 107

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1592
- Ceres seq\_id 1500690
- Location of start within SEQ ID NO 1589: at 452 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12602
- gi No. 3941468
- % Identity 98.4



- Alignment Length 249
- Location of Alignment in SEQ ID NO 1592: from 1 to 148

Maximum Length Sequence corresponding to clone ID 267357

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1593
- Ceres seq\_id 1500693

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1594
- Ceres seq\_id 1500694
- Location of start within SEQ ID NO 1593: at 68 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12603
- Ribosomal protein L36e
- Location within SEQ ID NO 1594: from 6 to 93 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12604
- gi No. 3236242
- % Identity 83.9
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1594: from 1 to 102

Maximum Length Sequence corresponding to clone ID 267559

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1595
- Ceres seq\_id 1500695

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1596
- Ceres seq\_id 1500696
- Location of start within SEQ ID NO 1595: at 228 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12605
- gi No. 4680201
- % Identity 70.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1596: from 11 to 98

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1597
- Ceres seq\_id 1500697
- Location of start within SEQ ID NO 1595: at 252 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12606
- gi No. 4680201
- % Identity 70.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1597: from 3 to 90

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1598
- Ceres seq\_id 1500698
- Location of start within SEQ ID NO 1595: at 255 nt.

#### (D) Related Amino Acid Sequences

- Maximum Length Sequence corresponding to clone ID 268117

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- Pat. Appln. SEQ ID NO 1599
- Ceres seq_id 1500703
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- Pat. Appln. SEQ ID NO 1600
- Ceres seq_id 1500704
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- #### (D) Related Amino Acid Sequences

- Pat. Appln. SEQ ID NO 1601  
- Ceres seq\_id 1500705

- (D) Related Amino Acid Sequences

- Pat. Appln. SEQ ID NO 1602  
- Ceres seq id 1500706

- #### (D) Related Amino Acid Sequences

- Maximum Length Sequence corresponding to clone ID 268199

- Pat. Appln. SEQ ID NO 1603  
- Ceres seq id 1500707

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1604
- Ceres seq\_id 1500708
- Location of start within SEQ ID NO 1603: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12611
- Asparaginase
- Location within SEQ ID NO 1604: from 20 to 182 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1605
- Ceres seq\_id 1500709
- Location of start within SEQ ID NO 1603: at 55 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12612
- Asparaginase
- Location within SEQ ID NO 1605: from 2 to 164 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1606
- Ceres seq\_id 1500710
- Location of start within SEQ ID NO 1603: at 292 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12613
- Asparaginase
- Location within SEQ ID NO 1606: from 1 to 85 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 268536

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1607
- Ceres seq\_id 1500719

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1608
- Ceres seq\_id 1500720
- Location of start within SEQ ID NO 1607: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12614
- Hsp20/alpha crystallin family
- Location within SEQ ID NO 1608: from 117 to 222 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1609
- Ceres seq\_id 1500721
- Location of start within SEQ ID NO 1607: at 39 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12615
- Hsp20/alpha crystallin family
- Location within SEQ ID NO 1609: from 105 to 210 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1610
- Ceres seq\_id 1500722
- Location of start within SEQ ID NO 1607: at 285 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12616
- Hsp20/alpha crystallin family
- Location within SEQ ID NO 1610: from 23 to 128 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 268621

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1611
- Ceres seq\_id 1500734

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1612
- Ceres seq\_id 1500735
- Location of start within SEQ ID NO 1611: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12617
- gi No. 4337197
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1612: from 23 to 78

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1613
- Ceres seq\_id 1500736
- Location of start within SEQ ID NO 1611: at 69 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12618
- gi No. 4337197
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1613: from 1 to 56

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1614
- Ceres seq\_id 1500737
- Location of start within SEQ ID NO 1611: at 87 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12619
- gi No. 4337197
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1614: from 1 to 50

Maximum Length Sequence corresponding to clone ID 268835

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1615
- Ceres seq\_id 1500742

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1616
- Ceres seq\_id 1500743
- Location of start within SEQ ID NO 1615: at 77 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12620
- gi No. 3510256
- % Identity 98.9
- Alignment Length 174
- Location of Alignment in SEQ ID NO 1616: from 1 to 174

Maximum Length Sequence corresponding to clone ID 268982

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1617
- Ceres seq\_id 1500748

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1618
- Ceres seq\_id 1500749
- Location of start within SEQ ID NO 1617: at 92 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12621
- Core histone H2A/H2B/H3/H4
- Location within SEQ ID NO 1618: from 17 to 135 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12622
- gi No. 10253
- % Identity 89
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
- Alignment No. 12623
- gi No. 103198
- % Identity 91.2
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
- Alignment No. 12624
- gi No. 104698
- % Identity 92
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1618: from 2 to 26
- Alignment No. 12625
- gi No. 1053045
- % Identity 95.3

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- Alignment Length 127
- Location of Alignment in SEQ ID NO 1618: from 1 to 127
  
- Alignment No. 12626
- gi No. 1053047
- % Identity 95.3
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1618: from 1 to 127
  
- Alignment No. 12627
- gi No. 1053053
- % Identity 91.3
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1618: from 1 to 127
  
- Alignment No. 12628
- gi No. 1053055
- % Identity 86.2
- Alignment Length 29
- Location of Alignment in SEQ ID NO 1618: from 1 to 29
  
- Alignment No. 12629
- gi No. 1053057
- % Identity 95.3
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1618: from 1 to 127
  
- Alignment No. 12630
- gi No. 1053059
- % Identity 93.7
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1618: from 1 to 127
  
- Alignment No. 12631
- gi No. 1076583
- % Identity 95
- Alignment Length 60
- Location of Alignment in SEQ ID NO 1618: from 1 to 60
  
- Alignment No. 12632
- gi No. 1079199
- % Identity 90.4
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12633
- gi No. 1085857
- % Identity 91.6
- Alignment Length 83
- Location of Alignment in SEQ ID NO 1618: from 34 to 116
  
- Alignment No. 12634
- gi No. 1085858
- % Identity 91.6
- Alignment Length 83
- Location of Alignment in SEQ ID NO 1618: from 34 to 116
  
- Alignment No. 12635
- gi No. 108593
- % Identity 76.2
- Alignment Length 21

- Location of Alignment in SEQ ID NO 1618: from 112 to 132
- Alignment No. 12636
- gi No. 109977
- % Identity 91.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1618: from 2 to 36
- Alignment No. 12637
- gi No. 1166436
- % Identity 81.4
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1618: from 36 to 94
- Alignment No. 12638
- gi No. 1197519
- % Identity 85.5
- Alignment Length 124
- Location of Alignment in SEQ ID NO 1618: from 13 to 136
- Alignment No. 12639
- gi No. 1208642
- % Identity 94.6
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1618: from 25 to 80
- Alignment No. 12640
- gi No. 1208644
- % Identity 94.6
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1618: from 25 to 80
- Alignment No. 12641
- gi No. 1208646
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1618: from 25 to 80
- Alignment No. 12642
- gi No. 1208656
- % Identity 94.6
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1618: from 25 to 80
- Alignment No. 12643
- gi No. 1208658
- % Identity 94.6
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1618: from 25 to 80
- Alignment No. 12644
- gi No. 1208664
- % Identity 94.6
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1618: from 25 to 80
- Alignment No. 12645
- gi No. 1208668
- % Identity 92.9
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1618: from 25 to 80

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- Alignment No. 12646
- gi No. 1208699
- % Identity 94.6
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1618: from 25 to 80
  
- Alignment No. 12647
- gi No. 1208701
- % Identity 94.6
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1618: from 25 to 80
  
- Alignment No. 12648
- gi No. 1208707
- % Identity 94.6
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1618: from 25 to 80
  
- Alignment No. 12649
- gi No. 1208715
- % Identity 94.6
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1618: from 25 to 80
  
- Alignment No. 12650
- gi No. 1208725
- % Identity 94.6
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1618: from 25 to 80
  
- Alignment No. 12651
- gi No. 1208727
- % Identity 94.6
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1618: from 25 to 80
  
- Alignment No. 12652
- gi No. 1213291
- % Identity 94.6
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1618: from 25 to 80
  
- Alignment No. 12653
- gi No. 1213307
- % Identity 94.6
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1618: from 25 to 80
  
- Alignment No. 12654
- gi No. 1213313
- % Identity 94.6
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1618: from 25 to 80
  
- Alignment No. 12655
- gi No. 1213315
- % Identity 89.3
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1618: from 25 to 80



- Alignment No. 12656
- gi No. 122065
- % Identity 86
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12657
- gi No. 122066
- % Identity 84.4
- Alignment Length 135
- Location of Alignment in SEQ ID NO 1618: from 1 to 135
  
- Alignment No. 12658
- gi No. 122068
- % Identity 91.9
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12659
- gi No. 122070
- % Identity 92.6
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12660
- gi No. 122071
- % Identity 85.4
- Alignment Length 41
- Location of Alignment in SEQ ID NO 1618: from 1 to 41
  
- Alignment No. 12661
- gi No. 122072
- % Identity 80.5
- Alignment Length 41
- Location of Alignment in SEQ ID NO 1618: from 1 to 41
  
- Alignment No. 12662
- gi No. 122074
- % Identity 88.2
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12663
- gi No. 122076
- % Identity 85.3
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12664
- gi No. 122077
- % Identity 84.6
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12665
- gi No. 122078
- % Identity 77.9
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12666

- gi No. 122079
- % Identity 91.9
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12667
- gi No. 122080
- % Identity 83.8
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12668
- gi No. 122081
- % Identity 90.4
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12669
- gi No. 122082
- % Identity 90.4
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12670
- gi No. 122083
- % Identity 93.3
- Alignment Length 135
- Location of Alignment in SEQ ID NO 1618: from 2 to 136
  
- Alignment No. 12671
- gi No. 122084
- % Identity 96.3
- Alignment Length 80
- Location of Alignment in SEQ ID NO 1618: from 57 to 136
  
- Alignment No. 12672
- gi No. 122085
- % Identity 94.1
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12673
- gi No. 122086
- % Identity 83.7
- Alignment Length 135
- Location of Alignment in SEQ ID NO 1618: from 1 to 135
  
- Alignment No. 12674
- gi No. 122087
- % Identity 94.1
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12675
- gi No. 122088
- % Identity 91.2
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12676
- gi No. 122089

- % Identity 90.4
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12677
- gi No. 122090
- % Identity 92.6
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12678
- gi No. 122091
- % Identity 83.1
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12679
- gi No. 1360625
- % Identity 79.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 1618: from 1 to 135
  
- Alignment No. 12680
- gi No. 1360627
- % Identity 77.6
- Alignment Length 98
- Location of Alignment in SEQ ID NO 1618: from 1 to 96
  
- Alignment No. 12681
- gi No. 1362108
- % Identity 93.4
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12682
- gi No. 1362171
- % Identity 90.6
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1618: from 105 to 136
  
- Alignment No. 12683
- gi No. 159967
- % Identity 89.7
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12684
- gi No. 161319
- % Identity 90.4
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12685
- gi No. 166384
- % Identity 93.4
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12686
- gi No. 1708108
- % Identity 91.9

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- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12687
- gi No. 1708109
- % Identity 91.2
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12688
- gi No. 171637
- % Identity 87.9
- Alignment Length 33
- Location of Alignment in SEQ ID NO 1618: from 3 to 35
  
- Alignment No. 12689
- gi No. 1723293
- % Identity 91.2
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1618: from 46 to 136
  
- Alignment No. 12690
- gi No. 1731925
- % Identity 91.3
- Alignment Length 115
- Location of Alignment in SEQ ID NO 1618: from 3 to 117
  
- Alignment No. 12691
- gi No. 1762791
- % Identity 71.4
- Alignment Length 140
- Location of Alignment in SEQ ID NO 1618: from 4 to 136
  
- Alignment No. 12692
- gi No. 1763308
- % Identity 83.8
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12693
- gi No. 1870700
- % Identity 91.9
- Alignment Length 111
- Location of Alignment in SEQ ID NO 1618: from 1 to 111
  
- Alignment No. 12694
- gi No. 1881589
- % Identity 89.6
- Alignment Length 48
- Location of Alignment in SEQ ID NO 1618: from 89 to 136
  
- Alignment No. 12695
- gi No. 1881594
- % Identity 91
- Alignment Length 89
- Location of Alignment in SEQ ID NO 1618: from 1 to 87
  
- Alignment No. 12696
- gi No. 1881601
- % Identity 93.1
- Alignment Length 87

- Location of Alignment in SEQ ID NO 1618: from 1 to 87
- Alignment No. 12697
- gi No. 19611
- % Identity 94.3
- Alignment Length 123
- Location of Alignment in SEQ ID NO 1618: from 14 to 136
- Alignment No. 12698
- gi No. 19614
- % Identity 93.1
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1618: from 79 to 136
- Alignment No. 12699
- gi No. 208461
- % Identity 84.2
- Alignment Length 19
- Location of Alignment in SEQ ID NO 1618: from 17 to 35
- Alignment No. 12700
- gi No. 208463
- % Identity 87.9
- Alignment Length 33
- Location of Alignment in SEQ ID NO 1618: from 3 to 35
- Alignment No. 12701
- gi No. 2116601
- % Identity 90.4
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
- Alignment No. 12702
- gi No. 211855
- % Identity 91.2
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
- Alignment No. 12703
- gi No. 2119011
- % Identity 91.2
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
- Alignment No. 12704
- gi No. 2119012
- % Identity 90.4
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
- Alignment No. 12705
- gi No. 2119013
- % Identity 91.9
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
- Alignment No. 12706
- gi No. 2119014
- % Identity 92.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1618: from 61 to 136

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- Alignment No. 12707
- gi No. 2119018
- % Identity 91.9
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12708
- gi No. 2135356
- % Identity 92.6
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1618: from 1 to 27
  
- Alignment No. 12709
- gi No. 2136686
- % Identity 93.1
- Alignment Length 29
- Location of Alignment in SEQ ID NO 1618: from 2 to 30
  
- Alignment No. 12710
- gi No. 2147399
- % Identity 92.3
- Alignment Length 39
- Location of Alignment in SEQ ID NO 1618: from 1 to 39
  
- Alignment No. 12711
- gi No. 2252516
- % Identity 92.1
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1618: from 1 to 38
  
- Alignment No. 12712
- gi No. 2253166
- % Identity 87.1
- Alignment Length 62
- Location of Alignment in SEQ ID NO 1618: from 1 to 62
  
- Alignment No. 12713
- gi No. 2253615
- % Identity 79.1
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12714
- gi No. 2909431
- % Identity 82.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1618: from 13 to 122
  
- Alignment No. 12715
- gi No. 2995213
- % Identity 71.1
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1618: from 1 to 36
  
- Alignment No. 12716
- gi No. 2995216
- % Identity 80.6
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1618: from 1 to 36

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- Alignment No. 12717
- gi No. 2995219
- % Identity 77.8
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1618: from 1 to 36
  
- Alignment No. 12718
- gi No. 2995225
- % Identity 86.1
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1618: from 1 to 36
  
- Alignment No. 12719
- gi No. 2995264
- % Identity 83.3
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1618: from 1 to 36
  
- Alignment No. 12720
- gi No. 3002595
- % Identity 91.2
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1618: from 15 to 105
  
- Alignment No. 12721
- gi No. 3002597
- % Identity 90.1
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1618: from 15 to 105
  
- Alignment No. 12722
- gi No. 3002603
- % Identity 88
- Alignment Length 92
- Location of Alignment in SEQ ID NO 1618: from 15 to 105
  
- Alignment No. 12723
- gi No. 3002613
- % Identity 89
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1618: from 15 to 105
  
- Alignment No. 12724
- gi No. 3002621
- % Identity 87.9
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1618: from 15 to 105
  
- Alignment No. 12725
- gi No. 3002633
- % Identity 90.1
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1618: from 15 to 105
  
- Alignment No. 12726
- gi No. 3002635
- % Identity 90.1
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1618: from 15 to 105
  
- Alignment No. 12727

- gi No. 3002637
- % Identity 90
- Alignment Length 90
- Location of Alignment in SEQ ID NO 1618: from 16 to 105
  
- Alignment No. 12728
- gi No. 3002643
- % Identity 90.1
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1618: from 15 to 105
  
- Alignment No. 12729
- gi No. 3002647
- % Identity 91.1
- Alignment Length 90
- Location of Alignment in SEQ ID NO 1618: from 15 to 104
  
- Alignment No. 12730
- gi No. 3002649
- % Identity 88.8
- Alignment Length 89
- Location of Alignment in SEQ ID NO 1618: from 15 to 103
  
- Alignment No. 12731
- gi No. 3002657
- % Identity 90.1
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1618: from 15 to 105
  
- Alignment No. 12732
- gi No. 3002663
- % Identity 89
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1618: from 15 to 105
  
- Alignment No. 12733
- gi No. 3219788
- % Identity 84.8
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1618: from 13 to 122
  
- Alignment No. 12734
- gi No. 3219789
- % Identity 83.9
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1618: from 13 to 122
  
- Alignment No. 12735
- gi No. 3219790
- % Identity 85.5
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1618: from 13 to 122
  
- Alignment No. 12736
- gi No. 3219791
- % Identity 84.8
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1618: from 13 to 122
  
- Alignment No. 12737
- gi No. 3219792

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- % Identity 83.9
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1618: from 13 to 122
  
- Alignment No. 12738
- gi No. 3219803
- % Identity 83
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1618: from 13 to 122
  
- Alignment No. 12739
- gi No. 3219805
- % Identity 81.1
- Alignment Length 111
- Location of Alignment in SEQ ID NO 1618: from 13 to 122
  
- Alignment No. 12740
- gi No. 352175
- % Identity 84.3
- Alignment Length 134
- Location of Alignment in SEQ ID NO 1618: from 2 to 135
  
- Alignment No. 12741
- gi No. 3745758
- % Identity 91.4
- Alignment Length 116
- Location of Alignment in SEQ ID NO 1618: from 21 to 136
  
- Alignment No. 12742
- gi No. 386772
- % Identity 91.8
- Alignment Length 134
- Location of Alignment in SEQ ID NO 1618: from 1 to 134
  
- Alignment No. 12743
- gi No. 3875420
- % Identity 84.6
- Alignment Length 123
- Location of Alignment in SEQ ID NO 1618: from 13 to 135
  
- Alignment No. 12744
- gi No. 3875421
- % Identity 75.6
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1618: from 1 to 127
  
- Alignment No. 12745
- gi No. 3880527
- % Identity 88.2
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12746
- gi No. 3880606
- % Identity 85
- Alignment Length 80
- Location of Alignment in SEQ ID NO 1618: from 57 to 136
  
- Alignment No. 12747
- gi No. 3979986
- % Identity 91.9

- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12748
- gi No. 404466
- % Identity 90.4
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12749
- gi No. 4139869
- % Identity 91.4
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1618: from 44 to 136
  
- Alignment No. 12750
- gi No. 417103
- % Identity 95.6
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12751
- gi No. 422605
- % Identity 88.2
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12752
- gi No. 422606
- % Identity 91.2
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12753
- gi No. 4388695
- % Identity 90.8
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1618: from 61 to 136
  
- Alignment No. 12754
- gi No. 4504279
- % Identity 91.2
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12755
- gi No. 4504281
- % Identity 91.9
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12756
- gi No. 4504283
- % Identity 91.2
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12757
- gi No. 4504299
- % Identity 89
- Alignment Length 136

- Location of Alignment in SEQ ID NO 1618: from 1 to 136
- Alignment No. 12758
- gi No. 4574208
- % Identity 96.5
- Alignment Length 115
- Location of Alignment in SEQ ID NO 1618: from 22 to 136
- Alignment No. 12759
- gi No. 4761212
- % Identity 91.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1618: from 8 to 119
- Alignment No. 12760
- gi No. 484441
- % Identity 91.2
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
- Alignment No. 12761
- gi No. 484530
- % Identity 89.6
- Alignment Length 135
- Location of Alignment in SEQ ID NO 1618: from 2 to 136
- Alignment No. 12762
- gi No. 484531
- % Identity 88.9
- Alignment Length 135
- Location of Alignment in SEQ ID NO 1618: from 2 to 136
- Alignment No. 12763
- gi No. 4883733
- % Identity 90.6
- Alignment Length 106
- Location of Alignment in SEQ ID NO 1618: from 11 to 116
- Alignment No. 12764
- gi No. 4883734
- % Identity 91.6
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1618: from 10 to 116
- Alignment No. 12765
- gi No. 4883735
- % Identity 91.7
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1618: from 9 to 117
- Alignment No. 12766
- gi No. 4883736
- % Identity 90.5
- Alignment Length 105
- Location of Alignment in SEQ ID NO 1618: from 11 to 115
- Alignment No. 12767
- gi No. 4883737
- % Identity 91.3
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1618: from 13 to 115

- Alignment No. 12768
- gi No. 4883738
- % Identity 87.1
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1618: from 17 to 109
  
- Alignment No. 12769
- gi No. 4883739
- % Identity 91.3
- Alignment Length 104
- Location of Alignment in SEQ ID NO 1618: from 13 to 116
  
- Alignment No. 12770
- gi No. 4883740
- % Identity 90.3
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1618: from 13 to 115
  
- Alignment No. 12771
- gi No. 4883741
- % Identity 91.7
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1618: from 9 to 116
  
- Alignment No. 12772
- gi No. 4883743
- % Identity 89
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1618: from 9 to 117
  
- Alignment No. 12773
- gi No. 4883744
- % Identity 90.8
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1618: from 9 to 117
  
- Alignment No. 12774
- gi No. 4883745
- % Identity 91.7
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1618: from 9 to 116
  
- Alignment No. 12775
- gi No. 4883746
- % Identity 89.8
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1618: from 9 to 116
  
- Alignment No. 12776
- gi No. 4883747
- % Identity 90.8
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1618: from 9 to 117
  
- Alignment No. 12777
- gi No. 4883748
- % Identity 90.8
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1618: from 9 to 117

- Alignment No. 12778
- gi No. 4883749
- % Identity 92.4
- Alignment Length 105
- Location of Alignment in SEQ ID NO 1618: from 13 to 117
  
- Alignment No. 12779
- gi No. 4883751
- % Identity 90.7
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1618: from 9 to 116
  
- Alignment No. 12780
- gi No. 4883752
- % Identity 90.7
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1618: from 10 to 117
  
- Alignment No. 12781
- gi No. 4883753
- % Identity 90.8
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1618: from 9 to 117
  
- Alignment No. 12782
- gi No. 4883754
- % Identity 89.7
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1618: from 9 to 115
  
- Alignment No. 12783
- gi No. 4883755
- % Identity 92.2
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1618: from 13 to 115
  
- Alignment No. 12784
- gi No. 4883756
- % Identity 90.8
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1618: from 9 to 117
  
- Alignment No. 12785
- gi No. 4883758
- % Identity 92.2
- Alignment Length 102
- Location of Alignment in SEQ ID NO 1618: from 13 to 114
  
- Alignment No. 12786
- gi No. 4883759
- % Identity 89.9
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1618: from 9 to 117
  
- Alignment No. 12787
- gi No. 4883760
- % Identity 89
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1618: from 9 to 117
  
- Alignment No. 12788

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- gi No. 4883762
- % Identity 89.8
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1618: from 9 to 116
  
- Alignment No. 12789
- gi No. 488571
- % Identity 95.3
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1618: from 10 to 136
  
- Alignment No. 12790
- gi No. 488573
- % Identity 96
- Alignment Length 124
- Location of Alignment in SEQ ID NO 1618: from 13 to 136
  
- Alignment No. 12791
- gi No. 529954
- % Identity 81.4
- Alignment Length 140
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12792
- gi No. 539427
- % Identity 91.7
- Alignment Length 48
- Location of Alignment in SEQ ID NO 1618: from 2 to 49
  
- Alignment No. 12793
- gi No. 556612
- % Identity 83.1
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12794
- gi No. 559807
- % Identity 87.5
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
  
- Alignment No. 12795
- gi No. 578470
- % Identity 90.3
- Alignment Length 72
- Location of Alignment in SEQ ID NO 1618: from 61 to 132
  
- Alignment No. 12796
- gi No. 630475
- % Identity 86.8
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1618: from 1 to 76
  
- Alignment No. 12797
- gi No. 630476
- % Identity 88.7
- Alignment Length 62
- Location of Alignment in SEQ ID NO 1618: from 1 to 62
  
- Alignment No. 12798
- gi No. 631693

- % Identity 91.4
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1618: from 79 to 136
  
- Alignment No. 12799
- gi No. 70743
- % Identity 91.9
- Alignment Length 135
- Location of Alignment in SEQ ID NO 1618: from 2 to 136
  
- Alignment No. 12800
- gi No. 70747
- % Identity 91.1
- Alignment Length 135
- Location of Alignment in SEQ ID NO 1618: from 2 to 136
  
- Alignment No. 12801
- gi No. 70748
- % Identity 90.4
- Alignment Length 135
- Location of Alignment in SEQ ID NO 1618: from 2 to 136
  
- Alignment No. 12802
- gi No. 70749
- % Identity 91.9
- Alignment Length 135
- Location of Alignment in SEQ ID NO 1618: from 2 to 136
  
- Alignment No. 12803
- gi No. 70753
- % Identity 94.1
- Alignment Length 135
- Location of Alignment in SEQ ID NO 1618: from 2 to 136
  
- Alignment No. 12804
- gi No. 70755
- % Identity 88.1
- Alignment Length 135
- Location of Alignment in SEQ ID NO 1618: from 2 to 136
  
- Alignment No. 12805
- gi No. 70760
- % Identity 77.8
- Alignment Length 135
- Location of Alignment in SEQ ID NO 1618: from 2 to 136
  
- Alignment No. 12806
- gi No. 729676
- % Identity 86.7
- Alignment Length 135
- Location of Alignment in SEQ ID NO 1618: from 1 to 135
  
- Alignment No. 12807
- gi No. 729677
- % Identity 83.7
- Alignment Length 135
- Location of Alignment in SEQ ID NO 1618: from 1 to 135
  
- Alignment No. 12808
- gi No. 81850
- % Identity 96.6

- Alignment Length 118
- Location of Alignment in SEQ ID NO 1618: from 19 to 136
- Alignment No. 12809
- gi No. 84300
- % Identity 82.9
- Alignment Length 41
- Location of Alignment in SEQ ID NO 1618: from 1 to 41
- Alignment No. 12810
- gi No. 84329
- % Identity 86.6
- Alignment Length 134
- Location of Alignment in SEQ ID NO 1618: from 2 to 135
- Alignment No. 12811
- gi No. 85000
- % Identity 92.2
- Alignment Length 115
- Location of Alignment in SEQ ID NO 1618: from 2 to 116
- Alignment No. 12812
- gi No. 85001
- % Identity 89.7
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
- Alignment No. 12813
- gi No. 90622
- % Identity 91.2
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
- Alignment No. 12814
- gi No. 995959
- % Identity 85
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1618: from 1 to 40
- Alignment No. 12815
- gi No. 99980
- % Identity 93.8
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1618: from 85 to 116
- Alignment No. 12816
- gi No. 99980
- % Identity 93.2
- Alignment Length 44
- Location of Alignment in SEQ ID NO 1618: from 2 to 45
- Alignment No. 12817
- gi No. 99981
- % Identity 94.1
- Alignment Length 51
- Location of Alignment in SEQ ID NO 1618: from 2 to 52

Maximum Length Sequence corresponding to clone ID 269337

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1619
- Ceres seq\_id 1500758



(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1620
- Ceres seq\_id 1500759
- Location of start within SEQ ID NO 1619: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12818
- Dihydroorotase-like
- Location within SEQ ID NO 1620: from 103 to 493 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1621
- Ceres seq\_id 1500760
- Location of start within SEQ ID NO 1619: at 19 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12819
- Dihydroorotase-like
- Location within SEQ ID NO 1621: from 97 to 487 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1622
- Ceres seq\_id 1500761
- Location of start within SEQ ID NO 1619: at 310 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12820
- Dihydroorotase-like
- Location within SEQ ID NO 1622: from 1 to 390 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 269402

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1623
- Ceres seq\_id 1500766

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1624
- Ceres seq\_id 1500767
- Location of start within SEQ ID NO 1623: at 519 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12821
- Fatty acid desaturase
- Location within SEQ ID NO 1624: from 1 to 111 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1625
- Ceres seq\_id 1500768
- Location of start within SEQ ID NO 1623: at 558 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12822
- Fatty acid desaturase
- Location within SEQ ID NO 1625: from 1 to 98 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1626
- Ceres seq\_id 1500769
- Location of start within SEQ ID NO 1623: at 582 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12823
- Fatty acid desaturase
- Location within SEQ ID NO 1626: from 1 to 90 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 269483

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1627
- Ceres seq\_id 1500778

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1628
- Ceres seq\_id 1500779
- Location of start within SEQ ID NO 1627: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12824
- Peroxidase
- Location within SEQ ID NO 1628: from 59 to 221 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12825
- gi No. 2342726
- % Identity 99.5
- Alignment Length 215
- Location of Alignment in SEQ ID NO 1628: from 7 to 221
- Alignment No. 12826
- gi No. 3643121
- % Identity 72.5
- Alignment Length 138
- Location of Alignment in SEQ ID NO 1628: from 84 to 221
- Alignment No. 12827
- gi No. 538502
- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1628: from 210 to 221

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1629
- Ceres seq\_id 1500780
- Location of start within SEQ ID NO 1627: at 19 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12828
- Peroxidase
- Location within SEQ ID NO 1629: from 53 to 215 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12829
- gi No. 2342726
- % Identity 99.5
- Alignment Length 215
- Location of Alignment in SEQ ID NO 1629: from 1 to 215
- Alignment No. 12830
- gi No. 3643121
- % Identity 72.5
- Alignment Length 138
- Location of Alignment in SEQ ID NO 1629: from 78 to 215
- Alignment No. 12831
- gi No. 538502
- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1629: from 204 to 215

Maximum Length Sequence corresponding to clone ID 269542

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1630
- Ceres seq\_id 1500785

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1631
- Ceres seq\_id 1500786
- Location of start within SEQ ID NO 1630: at 412 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12832
- gi No. 2827535
- % Identity 94.7
- Alignment Length 281
- Location of Alignment in SEQ ID NO 1631: from 1 to 172

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1632
- Ceres seq\_id 1500787
- Location of start within SEQ ID NO 1630: at 490 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12833
- gi No. 2827535
- % Identity 94.7
- Alignment Length 281
- Location of Alignment in SEQ ID NO 1632: from 1 to 146

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1633
- Ceres seq\_id 1500788
- Location of start within SEQ ID NO 1630: at 547 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12834
- gi No. 2827535
- % Identity 94.7
- Alignment Length 281
- Location of Alignment in SEQ ID NO 1633: from 1 to 127

Maximum Length Sequence corresponding to clone ID 269578

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1634
- Ceres seq\_id 1500793

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1635
- Ceres seq\_id 1500794
- Location of start within SEQ ID NO 1634: at 52 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12835
- gi No. 4220523
- % Identity 91.4
- Alignment Length 454
- Location of Alignment in SEQ ID NO 1635: from 1 to 254

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1636
- Ceres seq\_id 1500795
- Location of start within SEQ ID NO 1634: at 88 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12836
- gi No. 4220523
- % Identity 91.4
- Alignment Length 454
- Location of Alignment in SEQ ID NO 1636: from 1 to 242

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1637
- Ceres seq\_id 1500796
- Location of start within SEQ ID NO 1634: at 835 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12837
- gi No. 4220523
- % Identity 91.4
- Alignment Length 454
- Location of Alignment in SEQ ID NO 1637: from 1 to 179

Maximum Length Sequence corresponding to clone ID 269582

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1638
- Ceres seq\_id 1500797

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1639
- Ceres seq\_id 1500798
- Location of start within SEQ ID NO 1638: at 87 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12838
- Iron/Ascorbate oxidoreductase family
- Location within SEQ ID NO 1639: from 11 to 272 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1640
- Ceres seq\_id 1500799
- Location of start within SEQ ID NO 1638: at 420 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12839
- Iron/Ascorbate oxidoreductase family
- Location within SEQ ID NO 1640: from 1 to 161 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1641
- Ceres seq\_id 1500800
- Location of start within SEQ ID NO 1638: at 462 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12840
- Iron/Ascorbate oxidoreductase family
- Location within SEQ ID NO 1641: from 1 to 147 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 269610

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1642
- Ceres seq\_id 1500801

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1643
- Ceres seq\_id 1500802
- Location of start within SEQ ID NO 1642: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12841
- Polyprenyl synthetases
- Location within SEQ ID NO 1643: from 1 to 205 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12842
- gi No. 4836881
- % Identity 99.5
- Alignment Length 206
- Location of Alignment in SEQ ID NO 1643: from 1 to 205

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1644
- Ceres seq\_id 1500803
- Location of start within SEQ ID NO 1642: at 29 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12843
- Polyprenyl synthetases
- Location within SEQ ID NO 1644: from 1 to 196 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12844
- gi No. 4836881
- % Identity 99.5
- Alignment Length 206
- Location of Alignment in SEQ ID NO 1644: from 1 to 196

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1645
- Ceres seq\_id 1500804
- Location of start within SEQ ID NO 1642: at 80 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12845
- Polyprenyl synthetases
- Location within SEQ ID NO 1645: from 1 to 179 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12846
- gi No. 4836881
- % Identity 99.5
- Alignment Length 206
- Location of Alignment in SEQ ID NO 1645: from 1 to 179

Maximum Length Sequence corresponding to clone ID 269714

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1646
- Ceres seq\_id 1500805

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1647
- Ceres seq\_id 1500806
- Location of start within SEQ ID NO 1646: at 412 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12847
- gi No. 2832658
- % Identity 70
- Alignment Length 51
- Location of Alignment in SEQ ID NO 1647: from 81 to 129
  
- Alignment No. 12848
- gi No. 2832658
- % Identity 96.4
- Alignment Length 196
- Location of Alignment in SEQ ID NO 1647: from 198 to 389

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1648

- Ceres seq\_id 1500807
- Location of start within SEQ ID NO 1646: at 427 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12849
- gi No. 2832658
- % Identity 70
- Alignment Length 51
- Location of Alignment in SEQ ID NO 1648: from 76 to 124
  
- Alignment No. 12850
- gi No. 2832658
- % Identity 96.4
- Alignment Length 196
- Location of Alignment in SEQ ID NO 1648: from 193 to 384

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1649
- Ceres seq\_id 1500808
- Location of start within SEQ ID NO 1646: at 556 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12851
- gi No. 2832658
- % Identity 70
- Alignment Length 51
- Location of Alignment in SEQ ID NO 1649: from 33 to 81
  
- Alignment No. 12852
- gi No. 2832658
- % Identity 96.4
- Alignment Length 196
- Location of Alignment in SEQ ID NO 1649: from 150 to 341

Maximum Length Sequence corresponding to clone ID 269772

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1650
- Ceres seq\_id 1500809

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1651
- Ceres seq\_id 1500810
- Location of start within SEQ ID NO 1650: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 12853
- Glycosyl hydrolases family 17
- Location within SEQ ID NO 1651: from 59 to 179 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1652
- Ceres seq\_id 1500811
- Location of start within SEQ ID NO 1650: at 92 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12854
- Glycosyl hydrolases family 17
- Location within SEQ ID NO 1652: from 29 to 149 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 269883

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1653
- Ceres seq\_id 1500820

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1654
- Ceres seq\_id 1500821
- Location of start within SEQ ID NO 1653: at 87 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12855
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1654: from 20 to 192 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12856
- gi No. 2129698
- % Identity 84.5
- Alignment Length 187
- Location of Alignment in SEQ ID NO 1654: from 7 to 192

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1655
- Ceres seq\_id 1500822
- Location of start within SEQ ID NO 1653: at 111 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12857
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1655: from 12 to 184 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12858
- gi No. 2129698
- % Identity 84.5
- Alignment Length 187
- Location of Alignment in SEQ ID NO 1655: from 1 to 184

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1656
- Ceres seq\_id 1500823
- Location of start within SEQ ID NO 1653: at 297 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12859
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1656: from 1 to 122 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12860



- gi No. 2129698
- % Identity 84.5
- Alignment Length 187
- Location of Alignment in SEQ ID NO 1656: from 1 to 122

Maximum Length Sequence corresponding to clone ID 270032

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1657
- Ceres seq\_id 1500828

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1658
- Ceres seq\_id 1500829
- Location of start within SEQ ID NO 1657: at 309 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12861
- EPSP synthase (3-phosphoshikimate 1-carboxyvinyltransferase)
- Location within SEQ ID NO 1658: from 27 to 458 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12862
- gi No. 114165
- % Identity 77.1
- Alignment Length 493
- Location of Alignment in SEQ ID NO 1658: from 1 to 464
  
- Alignment No. 12863
- gi No. 114167
- % Identity 84.9
- Alignment Length 338
- Location of Alignment in SEQ ID NO 1658: from 127 to 464
  
- Alignment No. 12864
- gi No. 114171
- % Identity 91.3
- Alignment Length 508
- Location of Alignment in SEQ ID NO 1658: from 1 to 464
  
- Alignment No. 12865
- gi No. 114174
- % Identity 77.9
- Alignment Length 493
- Location of Alignment in SEQ ID NO 1658: from 1 to 464
  
- Alignment No. 12866
- gi No. 114176
- % Identity 79.3
- Alignment Length 483
- Location of Alignment in SEQ ID NO 1658: from 1 to 464
  
- Alignment No. 12867
- gi No. 1351978
- % Identity 90.7
- Alignment Length 508
- Location of Alignment in SEQ ID NO 1658: from 1 to 464
  
- Alignment No. 12868
- gi No. 1524383
- % Identity 82.6
- Alignment Length 443

- Location of Alignment in SEQ ID NO 1658: from 22 to 464
- Alignment No. 12869
- gi No. 2583124
- % Identity 91.1
- Alignment Length 508
- Location of Alignment in SEQ ID NO 1658: from 1 to 464
- Alignment No. 12870
- gi No. 3410961
- % Identity 81.1
- Alignment Length 391
- Location of Alignment in SEQ ID NO 1658: from 74 to 464
- Alignment No. 12871
- gi No. 66618
- % Identity 90.9
- Alignment Length 508
- Location of Alignment in SEQ ID NO 1658: from 1 to 464
- Alignment No. 12872
- gi No. 66619
- % Identity 78.1
- Alignment Length 493
- Location of Alignment in SEQ ID NO 1658: from 1 to 464

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1659
- Ceres seq\_id 1500830
- Location of start within SEQ ID NO 1657: at 528 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12873
- EPSP synthase (3-phosphoshikimate 1-carboxyvinyltransferase)
- Location within SEQ ID NO 1659: from 1 to 385 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12874
- gi No. 114165
- % Identity 77.1
- Alignment Length 493
- Location of Alignment in SEQ ID NO 1659: from 1 to 391
- Alignment No. 12875
- gi No. 114167
- % Identity 84.9
- Alignment Length 338
- Location of Alignment in SEQ ID NO 1659: from 54 to 391
- Alignment No. 12876
- gi No. 114171
- % Identity 91.3
- Alignment Length 508
- Location of Alignment in SEQ ID NO 1659: from 1 to 391
- Alignment No. 12877
- gi No. 114174
- % Identity 77.9
- Alignment Length 493
- Location of Alignment in SEQ ID NO 1659: from 1 to 391

- Alignment No. 12878
- gi No. 114176
- % Identity 79.3
- Alignment Length 483
- Location of Alignment in SEQ ID NO 1659: from 1 to 391
  
- Alignment No. 12879
- gi No. 1351978
- % Identity 90.7
- Alignment Length 508
- Location of Alignment in SEQ ID NO 1659: from 1 to 391
  
- Alignment No. 12880
- gi No. 1524383
- % Identity 82.6
- Alignment Length 443
- Location of Alignment in SEQ ID NO 1659: from 1 to 391
  
- Alignment No. 12881
- gi No. 2583124
- % Identity 91.1
- Alignment Length 508
- Location of Alignment in SEQ ID NO 1659: from 1 to 391
  
- Alignment No. 12882
- gi No. 3410961
- % Identity 81.1
- Alignment Length 391
- Location of Alignment in SEQ ID NO 1659: from 1 to 391
  
- Alignment No. 12883
- gi No. 66618
- % Identity 90.9
- Alignment Length 508
- Location of Alignment in SEQ ID NO 1659: from 1 to 391
  
- Alignment No. 12884
- gi No. 66619
- % Identity 78.1
- Alignment Length 493
- Location of Alignment in SEQ ID NO 1659: from 1 to 391

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1660
- Ceres seq\_id 1500831
- Location of start within SEQ ID NO 1657: at 678 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12885
- EPSP synthase (3-phosphoshikimate 1-carboxyvinyltransferase)
- Location within SEQ ID NO 1660: from 1 to 335 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12886
- gi No. 114165
- % Identity 77.1
- Alignment Length 493
- Location of Alignment in SEQ ID NO 1660: from 1 to 341

- Alignment No. 12887
- gi No. 114167
- % Identity 84.9
- Alignment Length 338
- Location of Alignment in SEQ ID NO 1660: from 4 to 341
  
- Alignment No. 12888
- gi No. 114171
- % Identity 91.3
- Alignment Length 508
- Location of Alignment in SEQ ID NO 1660: from 1 to 341
  
- Alignment No. 12889
- gi No. 114174
- % Identity 77.9
- Alignment Length 493
- Location of Alignment in SEQ ID NO 1660: from 1 to 341
  
- Alignment No. 12890
- gi No. 114176
- % Identity 79.3
- Alignment Length 483
- Location of Alignment in SEQ ID NO 1660: from 1 to 341
  
- Alignment No. 12891
- gi No. 1351978
- % Identity 90.7
- Alignment Length 508
- Location of Alignment in SEQ ID NO 1660: from 1 to 341
  
- Alignment No. 12892
- gi No. 1524383
- % Identity 82.6
- Alignment Length 443
- Location of Alignment in SEQ ID NO 1660: from 1 to 341
  
- Alignment No. 12893
- gi No. 2583124
- % Identity 91.1
- Alignment Length 508
- Location of Alignment in SEQ ID NO 1660: from 1 to 341
  
- Alignment No. 12894
- gi No. 3410961
- % Identity 81.1
- Alignment Length 391
- Location of Alignment in SEQ ID NO 1660: from 1 to 341
  
- Alignment No. 12895
- gi No. 66618
- % Identity 90.9
- Alignment Length 508
- Location of Alignment in SEQ ID NO 1660: from 1 to 341
  
- Alignment No. 12896
- gi No. 66619
- % Identity 78.1
- Alignment Length 493
- Location of Alignment in SEQ ID NO 1660: from 1 to 341

Maximum Length Sequence corresponding to clone ID 270102

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1661
- Ceres seq\_id 1500832

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1662
- Ceres seq\_id 1500833
- Location of start within SEQ ID NO 1661: at 298 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12897
- UDP-glucoronosyl and UDP-glucosyl transferases
- Location within SEQ ID NO 1662: from 183 to 292 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12898
- gi No. 3582342
- % Identity 84.5
- Alignment Length 291
- Location of Alignment in SEQ ID NO 1662: from 2 to 292

- Alignment No. 12899

- gi No. 3582343

- % Identity 99.3

- Alignment Length 291

- Location of Alignment in SEQ ID NO 1662: from 2 to 292

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1663
- Ceres seq\_id 1500834
- Location of start within SEQ ID NO 1661: at 349 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12900
- UDP-glucoronosyl and UDP-glucosyl transferases
- Location within SEQ ID NO 1663: from 166 to 275 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12901
- gi No. 3582342
- % Identity 84.5
- Alignment Length 291
- Location of Alignment in SEQ ID NO 1663: from 1 to 275

- Alignment No. 12902

- gi No. 3582343

- % Identity 99.3

- Alignment Length 291

- Location of Alignment in SEQ ID NO 1663: from 1 to 275

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1664
- Ceres seq\_id 1500835
- Location of start within SEQ ID NO 1661: at 424 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12903
- UDP-glucoronosyl and UDP-glucosyl transferases
- Location within SEQ ID NO 1664: from 141 to 250 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12904
- gi No. 3582342
- % Identity 84.5
- Alignment Length 291
- Location of Alignment in SEQ ID NO 1664: from 1 to 250
- Alignment No. 12905
- gi No. 3582343
- % Identity 99.3
- Alignment Length 291
- Location of Alignment in SEQ ID NO 1664: from 1 to 250

Maximum Length Sequence corresponding to clone ID 270115

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1665
- Ceres seq\_id 1500836

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1666
- Ceres seq\_id 1500837
- Location of start within SEQ ID NO 1665: at 35 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12906
- pfkB family carbohydrate kinase
- Location within SEQ ID NO 1666: from 59 to 124 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1667
- Ceres seq\_id 1500838
- Location of start within SEQ ID NO 1665: at 275 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 270512

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1668
- Ceres seq\_id 1500847

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1669
- Ceres seq\_id 1500848
- Location of start within SEQ ID NO 1668: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12907
- gi No. 2341040
- % Identity 97
- Alignment Length 100
- Location of Alignment in SEQ ID NO 1669: from 12 to 111

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1670
- Ceres seq\_id 1500849

- Location of start within SEQ ID NO 1668: at 35 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12908
- gi No. 2341040
- % Identity 97
- Alignment Length 100
- Location of Alignment in SEQ ID NO 1670: from 1 to 100

Maximum Length Sequence corresponding to clone ID 270714

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1671
- Ceres seq\_id 1500854

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1672
- Ceres seq\_id 1500855
- Location of start within SEQ ID NO 1671: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12909
- gi No. 4115376
- % Identity 97.7
- Alignment Length 132
- Location of Alignment in SEQ ID NO 1672: from 1 to 132

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1673
- Ceres seq\_id 1500856
- Location of start within SEQ ID NO 1671: at 62 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12910
- gi No. 4115376
- % Identity 97.7
- Alignment Length 132
- Location of Alignment in SEQ ID NO 1673: from 1 to 112

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1674
- Ceres seq\_id 1500857
- Location of start within SEQ ID NO 1671: at 95 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12911
- gi No. 4115376
- % Identity 97.7
- Alignment Length 132
- Location of Alignment in SEQ ID NO 1674: from 1 to 101

Maximum Length Sequence corresponding to clone ID 271327

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1675
- Ceres seq\_id 1500862

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1676
- Ceres seq\_id 1500863
- Location of start within SEQ ID NO 1675: at 303 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12912
- gi No. 3063449
- % Identity 100
- Alignment Length 134
- Location of Alignment in SEQ ID NO 1676: from 1 to 103

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1677
- Ceres seq\_id 1500864
- Location of start within SEQ ID NO 1675: at 309 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12913
- gi No. 3063449
- % Identity 100
- Alignment Length 134
- Location of Alignment in SEQ ID NO 1677: from 1 to 101

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1678
- Ceres seq\_id 1500865
- Location of start within SEQ ID NO 1675: at 360 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12914
- gi No. 3063449
- % Identity 100
- Alignment Length 134
- Location of Alignment in SEQ ID NO 1678: from 1 to 84

Maximum Length Sequence corresponding to clone ID 271605

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1679
- Ceres seq\_id 1500866

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1680
- Ceres seq\_id 1500867
- Location of start within SEQ ID NO 1679: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12915
- gi No. 1350720
- % Identity 97.3
- Alignment Length 111
- Location of Alignment in SEQ ID NO 1680: from 25 to 135
- Alignment No. 12916



- gi No. 1710539
- % Identity 81
- Alignment Length 42
- Location of Alignment in SEQ ID NO 1680: from 114 to 155
- Alignment No. 12917
- gi No. 3885519
- % Identity 88.6
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1680: from 121 to 155

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1681
- Ceres seq\_id 1500868
- Location of start within SEQ ID NO 1679: at 69 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12918
- gi No. 1350720
- % Identity 97.3
- Alignment Length 111
- Location of Alignment in SEQ ID NO 1681: from 3 to 113
- Alignment No. 12919
- gi No. 1710539
- % Identity 81
- Alignment Length 42
- Location of Alignment in SEQ ID NO 1681: from 92 to 133
- Alignment No. 12920
- gi No. 3885519
- % Identity 88.6
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1681: from 99 to 133

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1682
- Ceres seq\_id 1500869
- Location of start within SEQ ID NO 1679: at 195 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12921
- gi No. 1350720
- % Identity 97.3
- Alignment Length 111
- Location of Alignment in SEQ ID NO 1682: from 1 to 71
- Alignment No. 12922
- gi No. 1710539
- % Identity 81
- Alignment Length 42
- Location of Alignment in SEQ ID NO 1682: from 50 to 91
- Alignment No. 12923
- gi No. 3885519
- % Identity 88.6
- Alignment Length 35

- Location of Alignment in SEQ ID NO 1682: from 57 to 91

Maximum Length Sequence corresponding to clone ID 272234

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1683
- Ceres seq\_id 1500877

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1684
- Ceres seq\_id 1500878
- Location of start within SEQ ID NO 1683: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12924
- Zinc-binding dehydrogenases
- Location within SEQ ID NO 1684: from 66 to 160 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1685
- Ceres seq\_id 1500879
- Location of start within SEQ ID NO 1683: at 125 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12925
- Zinc-binding dehydrogenases
- Location within SEQ ID NO 1685: from 25 to 119 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1686
- Ceres seq\_id 1500880
- Location of start within SEQ ID NO 1683: at 209 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12926
- Zinc-binding dehydrogenases
- Location within SEQ ID NO 1686: from 1 to 91 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 272243

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1687
- Ceres seq\_id 1500881

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1688
- Ceres seq\_id 1500882
- Location of start within SEQ ID NO 1687: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1689
- Ceres seq\_id 1500883

- Location of start within SEQ ID NO 1687: at 115 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12927
- Biotin-requiring enzymes
- Location within SEQ ID NO 1689: from 75 to 139 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12928
- gi No. 4210332
- % Identity 74.7
- Alignment Length 79
- Location of Alignment in SEQ ID NO 1689: from 61 to 139
- Alignment No. 12929
- gi No. 4455214
- % Identity 76.7
- Alignment Length 60
- Location of Alignment in SEQ ID NO 1689: from 72 to 131

Maximum Length Sequence corresponding to clone ID 272277

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1690
- Ceres seq\_id 1500884

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1691
- Ceres seq\_id 1500885
- Location of start within SEQ ID NO 1690: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1692
- Ceres seq\_id 1500886
- Location of start within SEQ ID NO 1690: at 63 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12930
- Mucin-like glycoprotein
- Location within SEQ ID NO 1692: from 25 to 90 aa.
- Alignment No. 12931
- Mucin-like glycoprotein
- Location within SEQ ID NO 1692: from 33 to 90 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1693
- Ceres seq\_id 1500887
- Location of start within SEQ ID NO 1690: at 275 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 272304

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1694
- Ceres seq\_id 1500888

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1695
- Ceres seq\_id 1500889
- Location of start within SEQ ID NO 1694: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12932
- Protein phosphatase 2C
- Location within SEQ ID NO 1695: from 133 to 195 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12933
- gi No. 1914851
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1695: from 57 to 68
- Alignment No. 12934
- gi No. 3281853
- % Identity 75
- Alignment Length 72
- Location of Alignment in SEQ ID NO 1695: from 126 to 196
- Alignment No. 12935
- gi No. 4808585
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1695: from 59 to 69

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1696
- Ceres seq\_id 1500890
- Location of start within SEQ ID NO 1694: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1697
- Ceres seq\_id 1500891
- Location of start within SEQ ID NO 1694: at 154 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12936
- Protein phosphatase 2C
- Location within SEQ ID NO 1697: from 82 to 144 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12937
- gi No. 1914851
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1697: from 6 to 17
- Alignment No. 12938

- gi No. 3281853
- % Identity 75
- Alignment Length 72
- Location of Alignment in SEQ ID NO 1697: from 75 to 145
- Alignment No. 12939
- gi No. 4808585
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1697: from 8 to 18

Maximum Length Sequence corresponding to clone ID 272501

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1698
- Ceres seq\_id 1500900

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1699
- Ceres seq\_id 1500901
- Location of start within SEQ ID NO 1698: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12940
- gi No. 2130028
- % Identity 87.5
- Alignment Length 64
- Location of Alignment in SEQ ID NO 1699: from 27 to 90
- Alignment No. 12941
- gi No. 2293568
- % Identity 93.7
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1699: from 28 to 90
- Alignment No. 12942
- gi No. 4530585
- % Identity 80.6
- Alignment Length 62
- Location of Alignment in SEQ ID NO 1699: from 29 to 90
- Alignment No. 12943
- gi No. 5541720
- % Identity 78
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1699: from 27 to 85

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1700
- Ceres seq\_id 1500902
- Location of start within SEQ ID NO 1698: at 80 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12944
- gi No. 2130028
- % Identity 87.5
- Alignment Length 64
- Location of Alignment in SEQ ID NO 1700: from 1 to 64

- Alignment No. 12945
- gi No. 2293568
- % Identity 93.7
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1700: from 2 to 64
  
- Alignment No. 12946
- gi No. 4530585
- % Identity 80.6
- Alignment Length 62
- Location of Alignment in SEQ ID NO 1700: from 3 to 64
  
- Alignment No. 12947
- gi No. 5541720
- % Identity 78
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1700: from 1 to 59

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1701
- Ceres seq\_id 1500903
- Location of start within SEQ ID NO 1698: at 286 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12948
- gi No. 3377850
- % Identity 70.7
- Alignment Length 82
- Location of Alignment in SEQ ID NO 1701: from 1 to 79

Maximum Length Sequence corresponding to clone ID 272512

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1702
- Ceres seq\_id 1500907

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1703
- Ceres seq\_id 1500908
- Location of start within SEQ ID NO 1702: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1704
- Ceres seq\_id 1500909
- Location of start within SEQ ID NO 1702: at 161 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12949
- gi No. 1531758
- % Identity 75
- Alignment Length 48
- Location of Alignment in SEQ ID NO 1704: from 6 to 52

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1705

- Ceres seq\_id 1500910
- Location of start within SEQ ID NO 1702: at 316 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12950
- gi No. 1531758
- % Identity 71.2
- Alignment Length 52
- Location of Alignment in SEQ ID NO 1705: from 1 to 49
  
- Alignment No. 12951
- gi No. 4803938
- % Identity 82.7
- Alignment Length 52
- Location of Alignment in SEQ ID NO 1705: from 1 to 49

Maximum Length Sequence corresponding to clone ID 275375

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1706
- Ceres seq\_id 1500915

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1707
- Ceres seq\_id 1500916
- Location of start within SEQ ID NO 1706: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12952
- gi No. 3157951
- % Identity 97.2
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1707: from 147 to 181

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1708
- Ceres seq\_id 1500917
- Location of start within SEQ ID NO 1706: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12953
- gi No. 462338
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1708: from 57 to 77

Maximum Length Sequence corresponding to clone ID 275391

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1709
- Ceres seq\_id 1500926

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1710
- Ceres seq\_id 1500927
- Location of start within SEQ ID NO 1709: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
  - Alignment No. 12954
  - gi No. 2665536
  - % Identity 90.5
  - Alignment Length 179
  - Location of Alignment in SEQ ID NO 1710: from 33 to 209

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1711
  - Ceres seq\_id 1500928
  - Location of start within SEQ ID NO 1709: at 227 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
  - Alignment No. 12955
  - gi No. 2665536
  - % Identity 90.5
  - Alignment Length 179
  - Location of Alignment in SEQ ID NO 1711: from 1 to 134

Maximum Length Sequence corresponding to clone ID 275392

- (A) Polynucleotide Sequence
  - Pat. Appln. SEQ ID NO 1712
  - Ceres seq\_id 1500929
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1713
  - Ceres seq\_id 1500930
  - Location of start within SEQ ID NO 1712: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12956
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 1713: from 21 to 101 aa.

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1714
  - Ceres seq\_id 1500931
  - Location of start within SEQ ID NO 1712: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1715
  - Ceres seq\_id 1500932
  - Location of start within SEQ ID NO 1712: at 154 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 275421

- (A) Polynucleotide Sequence
  - Pat. Appln. SEQ ID NO 1716
  - Ceres seq\_id 1500945
- (B) Polypeptide Sequence



- Pat. Appln. SEQ ID NO 1717
- Ceres seq\_id 1500946
- Location of start within SEQ ID NO 1716: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12957
- Hsp20/alpha crystallin family
- Location within SEQ ID NO 1717: from 34 to 126 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12958
- gi No. 3876261
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1717: from 113 to 126

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1718
- Ceres seq\_id 1500947
- Location of start within SEQ ID NO 1716: at 72 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12959
- Hsp20/alpha crystallin family
- Location within SEQ ID NO 1718: from 11 to 103 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12960
- gi No. 3876261
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1718: from 90 to 103

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1719
- Ceres seq\_id 1500948
- Location of start within SEQ ID NO 1716: at 116 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 275764

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1720
- Ceres seq\_id 1500953

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1721
- Ceres seq\_id 1500954
- Location of start within SEQ ID NO 1720: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12961
- Beta-ketoacyl synthase
- Location within SEQ ID NO 1721: from 93 to 172 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12962

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- gi No. 119784
- % Identity 75.4
- Alignment Length 118
- Location of Alignment in SEQ ID NO 1721: from 58 to 172
- Alignment No. 12963
- gi No. 294668
- % Identity 83.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 1721: from 78 to 172

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1722
- Ceres seq\_id 1500955
- Location of start within SEQ ID NO 1720: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1723
- Ceres seq\_id 1500956
- Location of start within SEQ ID NO 1720: at 133 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12964
- Beta-ketoacyl synthase
- Location within SEQ ID NO 1723: from 49 to 128 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12965
- gi No. 119784
- % Identity 75.4
- Alignment Length 118
- Location of Alignment in SEQ ID NO 1723: from 14 to 128
- Alignment No. 12966
- gi No. 294668
- % Identity 83.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 1723: from 34 to 128

Maximum Length Sequence corresponding to clone ID 276068

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1724
- Ceres seq\_id 1500963

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1725
- Ceres seq\_id 1500964
- Location of start within SEQ ID NO 1724: at 95 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1726
- Ceres seq\_id 1500965
- Location of start within SEQ ID NO 1724: at 113 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1727
- Ceres seq\_id 1500966
- Location of start within SEQ ID NO 1724: at 141 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12967
- Mucin-like glycoprotein
- Location within SEQ ID NO 1727: from 1 to 56 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 276186

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1728
- Ceres seq\_id 1500974

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1729
- Ceres seq\_id 1500975
- Location of start within SEQ ID NO 1728: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12968
- gi No. 2425066
- % Identity 100
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1729: from 61 to 81

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1730
- Ceres seq\_id 1500976
- Location of start within SEQ ID NO 1728: at 62 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1731
- Ceres seq\_id 1500977
- Location of start within SEQ ID NO 1728: at 146 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 279386

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1732
- Ceres seq\_id 1500985

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1733
- Ceres seq\_id 1500986

- Location of start within SEQ ID NO 1732: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1734
- Ceres seq\_id 1500987
- Location of start within SEQ ID NO 1732: at 209 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12969
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1734: from 12 to 77 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12970
- gi No. 1777312
- % Identity 71.4
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1734: from 1 to 77
- Alignment No. 12971
- gi No. 2980770
- % Identity 71.8
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1734: from 7 to 77
- Alignment No. 12972
- gi No. 3256035
- % Identity 70.1
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1734: from 1 to 77

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1735
- Ceres seq\_id 1500988
- Location of start within SEQ ID NO 1732: at 233 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12973
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1735: from 4 to 69 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12974
- gi No. 1777312
- % Identity 71.4
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1735: from 1 to 69
- Alignment No. 12975
- gi No. 2980770
- % Identity 71.8
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1735: from 1 to 69
- Alignment No. 12976

- gi No. 3256035
- % Identity 70.1
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1735: from 1 to 69

Maximum Length Sequence corresponding to clone ID 280780

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1736
- Ceres seq\_id 1500992

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1737
- Ceres seq\_id 1500993
- Location of start within SEQ ID NO 1736: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12977
- gi No. 1041702
- % Identity 77.8
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1737: from 92 to 153
- Alignment No. 12978
- gi No. 1778097
- % Identity 84.6
- Alignment Length 39
- Location of Alignment in SEQ ID NO 1737: from 92 to 130
- Alignment No. 12979
- gi No. 1778099
- % Identity 71.4
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1737: from 92 to 153
- Alignment No. 12980
- gi No. 1778101
- % Identity 71.4
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1737: from 92 to 153
- Alignment No. 12981
- gi No. 1778107
- % Identity 89.5
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1737: from 92 to 129
- Alignment No. 12982
- gi No. 1778109
- % Identity 90.9
- Alignment Length 33
- Location of Alignment in SEQ ID NO 1737: from 92 to 124
- Alignment No. 12983
- gi No. 1815681
- % Identity 73
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1737: from 92 to 153
- Alignment No. 12984
- gi No. 3461833

- % Identity 73
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1737: from 92 to 153
  
- Alignment No. 12985
- gi No. 3510538
- % Identity 71.4
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1737: from 92 to 153
  
- Alignment No. 12986
- gi No. 3510540
- % Identity 71.4
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1737: from 92 to 153
  
- Alignment No. 12987
- gi No. 4027897
- % Identity 73
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1737: from 92 to 153
  
- Alignment No. 12988
- gi No. 4027899
- % Identity 73
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1737: from 92 to 153
  
- Alignment No. 12989
- gi No. 4138914
- % Identity 71.4
- Alignment Length 65
- Location of Alignment in SEQ ID NO 1737: from 92 to 153
  
- Alignment No. 12990
- gi No. 4138916
- % Identity 71.4
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1737: from 92 to 153
  
- Alignment No. 12991
- gi No. 5524700
- % Identity 73
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1737: from 92 to 153
  
- Alignment No. 12992
- gi No. 5714392
- % Identity 71.4
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1737: from 92 to 153

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1738
- Ceres seq\_id 1500994
- Location of start within SEQ ID NO 1736: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1739
- Ceres seq\_id 1500995
- Location of start within SEQ ID NO 1736: at 79 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12993
- gi No. 1041702
- % Identity 77.8
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1739: from 66 to 127
- Alignment No. 12994
- gi No. 1778097
- % Identity 84.6
- Alignment Length 39
- Location of Alignment in SEQ ID NO 1739: from 66 to 104
- Alignment No. 12995
- gi No. 1778099
- % Identity 71.4
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1739: from 66 to 127
- Alignment No. 12996
- gi No. 1778101
- % Identity 71.4
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1739: from 66 to 127
- Alignment No. 12997
- gi No. 1778107
- % Identity 89.5
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1739: from 66 to 103
- Alignment No. 12998
- gi No. 1778109
- % Identity 90.9
- Alignment Length 33
- Location of Alignment in SEQ ID NO 1739: from 66 to 98
- Alignment No. 12999
- gi No. 1815681
- % Identity 73
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1739: from 66 to 127
- Alignment No. 13000
- gi No. 3461833
- % Identity 73
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1739: from 66 to 127
- Alignment No. 13001
- gi No. 3510538
- % Identity 71.4
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1739: from 66 to 127

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- Alignment No. 13002
- gi No. 3510540
- % Identity 71.4
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1739: from 66 to 127
  
- Alignment No. 13003
- gi No. 4027897
- % Identity 73
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1739: from 66 to 127
  
- Alignment No. 13004
- gi No. 4027899
- % Identity 73
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1739: from 66 to 127
  
- Alignment No. 13005
- gi No. 4138914
- % Identity 71.4
- Alignment Length 65
- Location of Alignment in SEQ ID NO 1739: from 66 to 127
  
- Alignment No. 13006
- gi No. 4138916
- % Identity 71.4
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1739: from 66 to 127
  
- Alignment No. 13007
- gi No. 5524700
- % Identity 73
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1739: from 66 to 127
  
- Alignment No. 13008
- gi No. 5714392
- % Identity 71.4
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1739: from 66 to 127

Maximum Length Sequence corresponding to clone ID 280829

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1740
- Ceres seq\_id 1501005

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1741
- Ceres seq\_id 1501006
- Location of start within SEQ ID NO 1740: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1742
- Ceres seq\_id 1501007
- Location of start within SEQ ID NO 1740: at 99 nt.

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(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13009
- Sugar (and other) transporter
- Location within SEQ ID NO 1742: from 33 to 111 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1743
- Ceres seq\_id 1501008
- Location of start within SEQ ID NO 1740: at 213 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13010
- Sugar (and other) transporter
- Location within SEQ ID NO 1743: from 1 to 73 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 280866

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1744
- Ceres seq\_id 1501016

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1745
- Ceres seq\_id 1501017
- Location of start within SEQ ID NO 1744: at 100 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13011
- Histone-like transcription factors (CBF/NF-Y) and archaeal histones.
- Location within SEQ ID NO 1745: from 10 to 73 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1746
- Ceres seq\_id 1501018
- Location of start within SEQ ID NO 1744: at 151 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13012
- Histone-like transcription factors (CBF/NF-Y) and archaeal histones.
- Location within SEQ ID NO 1746: from 1 to 56 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 281118

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1747
- Ceres seq\_id 1501023

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1748
- Ceres seq\_id 1501024
- Location of start within SEQ ID NO 1747: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1749
- Ceres seq\_id 1501025
- Location of start within SEQ ID NO 1747: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13013
- Lipase/Acylhydrolase with GDSL-like motif
- Location within SEQ ID NO 1749: from 96 to 148 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1750
- Ceres seq\_id 1501026
- Location of start within SEQ ID NO 1747: at 165 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13014
- Lipase/Acylhydrolase with GDSL-like motif
- Location within SEQ ID NO 1750: from 42 to 94 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 281313

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1751
- Ceres seq\_id 1501027

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1752
- Ceres seq\_id 1501028
- Location of start within SEQ ID NO 1751: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13015
- gi No. 3153821
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1752: from 38 to 48

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1753
- Ceres seq\_id 1501029
- Location of start within SEQ ID NO 1751: at 101 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 282233

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1754

- Ceres seq\_id 1501037
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1755
  - Ceres seq\_id 1501038
  - Location of start within SEQ ID NO 1754: at 148 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13016
- Adaptor complexes medium subunit family
- Location within SEQ ID NO 1755: from 8 to 121 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13017
- gi No. 2271477
- % Identity 95.9
- Alignment Length 122
- Location of Alignment in SEQ ID NO 1755: from 1 to 121

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1756
- Ceres seq\_id 1501039
- Location of start within SEQ ID NO 1754: at 238 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13018
- Adaptor complexes medium subunit family
- Location within SEQ ID NO 1756: from 1 to 91 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13019
- gi No. 2271477
- % Identity 95.9
- Alignment Length 122
- Location of Alignment in SEQ ID NO 1756: from 1 to 91

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1757
- Ceres seq\_id 1501040
- Location of start within SEQ ID NO 1754: at 256 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13020
- Adaptor complexes medium subunit family
- Location within SEQ ID NO 1757: from 1 to 85 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13021
- gi No. 2271477
- % Identity 95.9
- Alignment Length 122
- Location of Alignment in SEQ ID NO 1757: from 1 to 85

Maximum Length Sequence corresponding to clone ID 282427

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1758
- Ceres seq\_id 1501058

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1759

- Ceres seq\_id 1501059
- Location of start within SEQ ID NO 1758: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1760
- Ceres seq\_id 1501060
- Location of start within SEQ ID NO 1758: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13022
- Mucin-like glycoprotein
- Location within SEQ ID NO 1760: from 20 to 133 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1761
- Ceres seq\_id 1501061
- Location of start within SEQ ID NO 1758: at 91 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 282587

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1762
- Ceres seq\_id 1501090

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1763
- Ceres seq\_id 1501091
- Location of start within SEQ ID NO 1762: at 156 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13023
- BAH domain
- Location within SEQ ID NO 1763: from 30 to 115 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13024
- gi No. 3046693
- % Identity 78.2
- Alignment Length 87
- Location of Alignment in SEQ ID NO 1763: from 30 to 115

- Alignment No. 13025
- gi No. 3377844
- % Identity 76.1
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1763: from 29 to 115

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1764
- Ceres seq\_id 1501092
- Location of start within SEQ ID NO 1762: at 165 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13026
- BAH domain
- Location within SEQ ID NO 1764: from 27 to 112 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13027
- gi No. 3046693
- % Identity 78.2
- Alignment Length 87
- Location of Alignment in SEQ ID NO 1764: from 27 to 112
- Alignment No. 13028
- gi No. 3377844
- % Identity 76.1
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1764: from 26 to 112

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1765
- Ceres seq\_id 1501093
- Location of start within SEQ ID NO 1762: at 258 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13029
- BAH domain
- Location within SEQ ID NO 1765: from 1 to 81 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13030
- gi No. 3046693
- % Identity 78.2
- Alignment Length 87
- Location of Alignment in SEQ ID NO 1765: from 1 to 81
- Alignment No. 13031
- gi No. 3377844
- % Identity 76.1
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1765: from 1 to 81

Maximum Length Sequence corresponding to clone ID 282710

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1766
- Ceres seq\_id 1501115

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1767
- Ceres seq\_id 1501116
- Location of start within SEQ ID NO 1766: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13032
- gi No. 1742961
- % Identity 73.5
- Alignment Length 49
- Location of Alignment in SEQ ID NO 1767: from 43 to 91

- Alignment No. 13033
- gi No. 1791309
- % Identity 73.5
- Alignment Length 49
- Location of Alignment in SEQ ID NO 1767: from 43 to 91
  
- Alignment No. 13034
- gi No. 2198851
- % Identity 89
- Alignment Length 73
- Location of Alignment in SEQ ID NO 1767: from 33 to 105
  
- Alignment No. 13035
- gi No. 2198851
- % Identity 73.8
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1767: from 80 to 107
  
- Alignment No. 13036
- gi No. 2198853
- % Identity 89
- Alignment Length 73
- Location of Alignment in SEQ ID NO 1767: from 33 to 105
  
- Alignment No. 13037
- gi No. 2198853
- % Identity 73.8
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1767: from 80 to 107
  
- Alignment No. 13038
- gi No. 4959932
- % Identity 75.5
- Alignment Length 49
- Location of Alignment in SEQ ID NO 1767: from 45 to 91

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1768
- Ceres seq\_id 1501117
- Location of start within SEQ ID NO 1766: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1769
- Ceres seq\_id 1501118
- Location of start within SEQ ID NO 1766: at 97 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13039
- gi No. 1742961
- % Identity 73.5
- Alignment Length 49
- Location of Alignment in SEQ ID NO 1769: from 11 to 59
  
- Alignment No. 13040

- gi No. 1791309
- % Identity 73.5
- Alignment Length 49
- Location of Alignment in SEQ ID NO 1769: from 11 to 59
  
- Alignment No. 13041
- gi No. 2198851
- % Identity 89
- Alignment Length 73
- Location of Alignment in SEQ ID NO 1769: from 1 to 73
  
- Alignment No. 13042
- gi No. 2198851
- % Identity 73.8
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1769: from 48 to 75
  
- Alignment No. 13043
- gi No. 2198853
- % Identity 89
- Alignment Length 73
- Location of Alignment in SEQ ID NO 1769: from 1 to 73
  
- Alignment No. 13044
- gi No. 2198853
- % Identity 73.8
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1769: from 48 to 75
  
- Alignment No. 13045
- gi No. 4959932
- % Identity 75.5
- Alignment Length 49
- Location of Alignment in SEQ ID NO 1769: from 13 to 59

Maximum Length Sequence corresponding to clone ID 282723

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1770
- Ceres seq\_id 1501119

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1771
- Ceres seq\_id 1501120
- Location of start within SEQ ID NO 1770: at 239 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13046
- Clathrin adaptor complex small chain
- Location within SEQ ID NO 1771: from 1 to 76 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1772
- Ceres seq\_id 1501121
- Location of start within SEQ ID NO 1770: at 254 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13047
- Clathrin adaptor complex small chain

- Location within SEQ ID NO 1772: from 1 to 71 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1773
- Ceres seq\_id 1501122
- Location of start within SEQ ID NO 1770: at 492 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13048
- Clathrin adaptor complex small chain
- Location within SEQ ID NO 1773: from 1 to 63 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13049
- gi No. 4835237
- % Identity 72.2
- Alignment Length 79
- Location of Alignment in SEQ ID NO 1773: from 1 to 61

Maximum Length Sequence corresponding to clone ID 282725

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1774
- Ceres seq\_id 1501123

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1775
- Ceres seq\_id 1501124
- Location of start within SEQ ID NO 1774: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1776
- Ceres seq\_id 1501125
- Location of start within SEQ ID NO 1774: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13050
- gi No. 2688824
- % Identity 76.3
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1776: from 74 to 111

Maximum Length Sequence corresponding to clone ID 282757

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1777
- Ceres seq\_id 1501137

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1778
- Ceres seq\_id 1501138
- Location of start within SEQ ID NO 1777: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences



- Alignment No. 13051
- gi No. 103249
- % Identity 71
- Alignment Length 69
- Location of Alignment in SEQ ID NO 1778: from 90 to 157
  
- Alignment No. 13052
- gi No. 130831
- % Identity 71
- Alignment Length 69
- Location of Alignment in SEQ ID NO 1778: from 90 to 157
  
- Alignment No. 13053
- gi No. 1346784
- % Identity 77.6
- Alignment Length 67
- Location of Alignment in SEQ ID NO 1778: from 92 to 157
  
- Alignment No. 13054
- gi No. 2511580
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1778: from 89 to 157
  
- Alignment No. 13055
- gi No. 2529567
- % Identity 71
- Alignment Length 69
- Location of Alignment in SEQ ID NO 1778: from 90 to 157
  
- Alignment No. 13056
- gi No. 266839
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1778: from 89 to 157
  
- Alignment No. 13057
- gi No. 3024432
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1778: from 89 to 157
  
- Alignment No. 13058
- gi No. 3334299
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1778: from 89 to 157
  
- Alignment No. 13059
- gi No. 3421082
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1778: from 89 to 157
  
- Alignment No. 13060
- gi No. 3805978
- % Identity 77.6
- Alignment Length 67
- Location of Alignment in SEQ ID NO 1778: from 92 to 157
  
- Alignment No. 13061

- gi No. 3874776
- % Identity 71.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1778: from 89 to 157
  
- Alignment No. 13062
- gi No. 4092058
- % Identity 77.6
- Alignment Length 67
- Location of Alignment in SEQ ID NO 1778: from 92 to 157
  
- Alignment No. 13063
- gi No. 4506189
- % Identity 77.6
- Alignment Length 67
- Location of Alignment in SEQ ID NO 1778: from 92 to 157
  
- Alignment No. 13064
- gi No. 4586592
- % Identity 91.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1778: from 89 to 157
  
- Alignment No. 13065
- gi No. 464459
- % Identity 82.6
- Alignment Length 69
- Location of Alignment in SEQ ID NO 1778: from 90 to 157
  
- Alignment No. 13066
- gi No. 485265
- % Identity 77.6
- Alignment Length 67
- Location of Alignment in SEQ ID NO 1778: from 92 to 157

Maximum Length Sequence corresponding to clone ID 282828

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1779
- Ceres seq\_id 1501139

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1780
- Ceres seq\_id 1501140
- Location of start within SEQ ID NO 1779: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13067
- Fatty acid desaturase
- Location within SEQ ID NO 1780: from 93 to 144 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13068
- gi No. 2194093
- % Identity 71.7
- Alignment Length 46
- Location of Alignment in SEQ ID NO 1780: from 99 to 144
  
- Alignment No. 13069
- gi No. 533082
- % Identity 71.2
- Alignment Length 52

- Location of Alignment in SEQ ID NO 1780: from 93 to 144

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1781
- Ceres seq\_id 1501141
- Location of start within SEQ ID NO 1779: at 161 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13070
- Fatty acid desaturase
- Location within SEQ ID NO 1781: from 40 to 91 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13071
- gi No. 2194093
- % Identity 71.7
- Alignment Length 46
- Location of Alignment in SEQ ID NO 1781: from 46 to 91
- Alignment No. 13072
- gi No. 533082
- % Identity 71.2
- Alignment Length 52
- Location of Alignment in SEQ ID NO 1781: from 40 to 91

Maximum Length Sequence corresponding to clone ID 282832

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1782
- Ceres seq\_id 1501142

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1783
- Ceres seq\_id 1501143
- Location of start within SEQ ID NO 1782: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1784
- Ceres seq\_id 1501144
- Location of start within SEQ ID NO 1782: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1785
- Ceres seq\_id 1501145
- Location of start within SEQ ID NO 1782: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13073
- gi No. 2358287
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1785: from 38 to 48

- Alignment No. 13074
- gi No. 3928704
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1785: from 10 to 23
  
- Alignment No. 13075
- gi No. 4508019
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1785: from 10 to 23
  
- Alignment No. 13076
- gi No. 545067
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1785: from 139 to 151

Maximum Length Sequence corresponding to clone ID 282932

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1786
- Ceres seq\_id 1501163

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1787
- Ceres seq\_id 1501164
- Location of start within SEQ ID NO 1786: at 139 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13077
- Histone deacetylase family
- Location within SEQ ID NO 1787: from 26 to 113 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13078
- gi No. 3023945
- % Identity 83.2
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1787: from 8 to 113

- Alignment No. 13079
- gi No. 3023947
- % Identity 95.6
- Alignment Length 114
- Location of Alignment in SEQ ID NO 1787: from 1 to 113

- Alignment No. 13080
- gi No. 4467119
- % Identity 84.1
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1787: from 8 to 113

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1788
- Ceres seq\_id 1501165
- Location of start within SEQ ID NO 1786: at 268 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13081

- Histone deacetylase family
- Location within SEQ ID NO 1788: from 1 to 70 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13082
- gi No. 3023945
- % Identity 83.2
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1788: from 1 to 70
- Alignment No. 13083
- gi No. 3023947
- % Identity 95.6
- Alignment Length 114
- Location of Alignment in SEQ ID NO 1788: from 1 to 70
- Alignment No. 13084
- gi No. 4467119
- % Identity 84.1
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1788: from 1 to 70

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1789
- Ceres seq\_id 1501166
- Location of start within SEQ ID NO 1786: at 289 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13085
- Histone deacetylase family
- Location within SEQ ID NO 1789: from 1 to 63 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13086
- gi No. 3023945
- % Identity 83.2
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1789: from 1 to 63
- Alignment No. 13087
- gi No. 3023947
- % Identity 95.6
- Alignment Length 114
- Location of Alignment in SEQ ID NO 1789: from 1 to 63
- Alignment No. 13088
- gi No. 4467119
- % Identity 84.1
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1789: from 1 to 63

Maximum Length Sequence corresponding to clone ID 283094

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1790
- Ceres seq\_id 1501167

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1791
- Ceres seq\_id 1501168
- Location of start within SEQ ID NO 1790: at 3 nt.

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(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13089
- gi No. 1170404
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1791: from 46 to 58
- Alignment No. 13090
- gi No. 1170404
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1791: from 44 to 58

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1792
- Ceres seq\_id 1501169
- Location of start within SEQ ID NO 1790: at 30 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13091
- gi No. 1170404
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1792: from 37 to 49
- Alignment No. 13092
- gi No. 1170404
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1792: from 35 to 49

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1793
- Ceres seq\_id 1501170
- Location of start within SEQ ID NO 1790: at 186 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 283333

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1794
- Ceres seq\_id 1501203

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1795
- Ceres seq\_id 1501204
- Location of start within SEQ ID NO 1794: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1796
- Ceres seq\_id 1501205
- Location of start within SEQ ID NO 1794: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13093
- gi No. 102427
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1796: from 18 to 31
  
- Alignment No. 13094
- gi No. 102427
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1796: from 18 to 31
  
- Alignment No. 13095
- gi No. 4467884
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1796: from 19 to 29
  
- Alignment No. 13096
- gi No. 5123787
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 1796: from 17 to 31
  
- Alignment No. 13097
- gi No. 553165
- % Identity 92.9
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1796: from 18 to 31

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1797
- Ceres seq\_id 1501206
- Location of start within SEQ ID NO 1794: at 146 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 283840

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1798
- Ceres seq\_id 1501245

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1799
- Ceres seq\_id 1501246
- Location of start within SEQ ID NO 1798: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13098
- gi No. 322759
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1799: from 15 to 25

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1800
- Ceres seq\_id 1501247
- Location of start within SEQ ID NO 1798: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13099
- gi No. 688080
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1800: from 93 to 103
- Alignment No. 13100
- gi No. 688080
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1800: from 90 to 103

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1801
- Ceres seq\_id 1501248
- Location of start within SEQ ID NO 1798: at 226 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 283927

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1802
- Ceres seq\_id 1501259

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1803
- Ceres seq\_id 1501260
- Location of start within SEQ ID NO 1802: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13101
- gi No. 1082871
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1803: from 28 to 53
- Alignment No. 13102
- gi No. 1352426
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1803: from 28 to 53
- Alignment No. 13103
- gi No. 1352427
- % Identity 96.2
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1803: from 28 to 53
- Alignment No. 13104
- gi No. 1794151

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- % Identity 83.3
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1803: from 30 to 53
- Alignment No. 13105
- gi No. 2851524
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1803: from 28 to 53
- Alignment No. 13106
- gi No. 3024017
- % Identity 96.2
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1803: from 28 to 53
- Alignment No. 13107
- gi No. 3264536
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1803: from 28 to 53
- Alignment No. 13108
- gi No. 3746340
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1803: from 28 to 53
- Alignment No. 13109
- gi No. 3811355
- % Identity 75.9
- Alignment Length 29
- Location of Alignment in SEQ ID NO 1803: from 28 to 56
- Alignment No. 13110
- gi No. 4503499
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1803: from 28 to 53
- Alignment No. 13111
- gi No. 4587600
- % Identity 100
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1803: from 28 to 53
- Alignment No. 13112
- gi No. 4758254
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1803: from 28 to 53
- Alignment No. 13113
- gi No. 5690414
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1803: from 28 to 53
- Alignment No. 13114
- gi No. 626041
- % Identity 96

- Alignment Length 25
- Location of Alignment in SEQ ID NO 1803: from 29 to 53
- Alignment No. 13115
- gi No. 627817
- % Identity 84
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1803: from 29 to 53

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1804
- Ceres seq\_id 1501261
- Location of start within SEQ ID NO 1802: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13116
- gi No. 1082871
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1804: from 55 to 76
- Alignment No. 13117
- gi No. 1352426
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1804: from 55 to 76
- Alignment No. 13118
- gi No. 1352427
- % Identity 100
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1804: from 55 to 76
- Alignment No. 13119
- gi No. 1794151
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1804: from 55 to 76
- Alignment No. 13120
- gi No. 2851524
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1804: from 55 to 76
- Alignment No. 13121
- gi No. 3024017
- % Identity 95.5
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1804: from 55 to 76
- Alignment No. 13122
- gi No. 3264536
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1804: from 55 to 76
- Alignment No. 13123
- gi No. 3746340

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- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1804: from 55 to 76
  
- Alignment No. 13124
- gi No. 3811355
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1804: from 56 to 75
  
- Alignment No. 13125
- gi No. 4503499
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1804: from 55 to 76
  
- Alignment No. 13126
- gi No. 4587600
- % Identity 95.5
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1804: from 55 to 76
  
- Alignment No. 13127
- gi No. 4758254
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1804: from 55 to 76
  
- Alignment No. 13128
- gi No. 5690414
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1804: from 55 to 76
  
- Alignment No. 13129
- gi No. 626041
- % Identity 100
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1804: from 55 to 76
  
- Alignment No. 13130
- gi No. 627817
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1804: from 55 to 76
  
- Alignment No. 13131
- gi No. 729814
- % Identity 77.3
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1804: from 55 to 76

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1805
- Ceres seq\_id 1501262
- Location of start within SEQ ID NO 1802: at 83 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 13132

- gi No. 1082871
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1805: from 1 to 26
  
- Alignment No. 13133
- gi No. 1352426
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1805: from 1 to 26
  
- Alignment No. 13134
- gi No. 1352427
- % Identity 96.2
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1805: from 1 to 26
  
- Alignment No. 13135
- gi No. 1794151
- % Identity 83.3
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1805: from 3 to 26
  
- Alignment No. 13136
- gi No. 2851524
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1805: from 1 to 26
  
- Alignment No. 13137
- gi No. 3024017
- % Identity 96.2
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1805: from 1 to 26
  
- Alignment No. 13138
- gi No. 3264536
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1805: from 1 to 26
  
- Alignment No. 13139
- gi No. 3746340
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1805: from 1 to 26
  
- Alignment No. 13140
- gi No. 3811355
- % Identity 75.9
- Alignment Length 29
- Location of Alignment in SEQ ID NO 1805: from 1 to 29
  
- Alignment No. 13141
- gi No. 4503499
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1805: from 1 to 26
  
- Alignment No. 13142
- gi No. 4587600

- % Identity 100
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1805: from 1 to 26
  
- Alignment No. 13143
- gi No. 4758254
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1805: from 1 to 26
  
- Alignment No. 13144
- gi No. 5690414
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1805: from 1 to 26
  
- Alignment No. 13145
- gi No. 626041
- % Identity 96
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1805: from 2 to 26
  
- Alignment No. 13146
- gi No. 627817
- % Identity 84
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1805: from 2 to 26

Maximum Length Sequence corresponding to clone ID 283950

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1806
- Ceres seq\_id 1501268

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1807
- Ceres seq\_id 1501269
- Location of start within SEQ ID NO 1806: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13147
- gi No. 419789
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1807: from 146 to 158

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1808
- Ceres seq\_id 1501270
- Location of start within SEQ ID NO 1806: at 116 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13148
- Glycosyl hydrolases family 17
- Location within SEQ ID NO 1808: from 29 to 109 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 284027

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1809
- Ceres seq\_id 1501280
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1810
  - Ceres seq\_id 1501281
  - Location of start within SEQ ID NO 1809: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13149
  - gi No. 100931
  - % Identity 72.7
  - Alignment Length 22
  - Location of Alignment in SEQ ID NO 1810: from 44 to 64
- Alignment No. 13150
  - gi No. 1045052
  - % Identity 71.8
  - Alignment Length 39
  - Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13151
  - gi No. 1065516
  - % Identity 77.8
  - Alignment Length 36
  - Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13152
  - gi No. 1078809
  - % Identity 76
  - Alignment Length 25
  - Location of Alignment in SEQ ID NO 1810: from 38 to 62
- Alignment No. 13153
  - gi No. 1078810
  - % Identity 76
  - Alignment Length 25
  - Location of Alignment in SEQ ID NO 1810: from 38 to 62
- Alignment No. 13154
  - gi No. 1101025
  - % Identity 86.1
  - Alignment Length 36
  - Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13155
  - gi No. 1136120
  - % Identity 78.4
  - Alignment Length 37
  - Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13156
  - gi No. 1136122
  - % Identity 86.5
  - Alignment Length 37
  - Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13157
  - gi No. 1174592
  - % Identity 83.9

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- Alignment Length 31
- Location of Alignment in SEQ ID NO 1810: from 29 to 59
- Alignment No. 13158
- gi No. 1174593
- % Identity 71.1
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13159
- gi No. 1223784
- % Identity 77.1
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1810: from 29 to 63
- Alignment No. 13160
- gi No. 1223786
- % Identity 84.8
- Alignment Length 33
- Location of Alignment in SEQ ID NO 1810: from 29 to 57
- Alignment No. 13161
- gi No. 1245776
- % Identity 76.3
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13162
- gi No. 1279206
- % Identity 84.8
- Alignment Length 33
- Location of Alignment in SEQ ID NO 1810: from 29 to 61
- Alignment No. 13163
- gi No. 1334748
- % Identity 71.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1810: from 29 to 63
- Alignment No. 13164
- gi No. 1351200
- % Identity 78.1
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1810: from 29 to 60
- Alignment No. 13165
- gi No. 135391
- % Identity 83.3
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13166
- gi No. 135392
- % Identity 71.9
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1810: from 29 to 60
- Alignment No. 13167
- gi No. 135393
- % Identity 70.3
- Alignment Length 37

- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13168
- gi No. 135394
- % Identity 75.7
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13169
- gi No. 135395
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13170
- gi No. 135396
- % Identity 72.2
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13171
- gi No. 135398
- % Identity 83.8
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13172
- gi No. 135399
- % Identity 91.7
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13173
- gi No. 135400
- % Identity 78.9
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13174
- gi No. 135401
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13175
- gi No. 135402
- % Identity 71.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1810: from 29 to 63
- Alignment No. 13176
- gi No. 135404
- % Identity 75.7
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13177
- gi No. 135406
- % Identity 91.7
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64



- Alignment No. 13178
- gi No. 135407
- % Identity 73.5
- Alignment Length 34
- Location of Alignment in SEQ ID NO 1810: from 29 to 62
  
- Alignment No. 13179
- gi No. 135409
- % Identity 75.7
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13180
- gi No. 135411
- % Identity 81.1
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13181
- gi No. 135412
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13182
- gi No. 135413
- % Identity 77.8
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1810: from 29 to 55
  
- Alignment No. 13183
- gi No. 135414
- % Identity 84.4
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1810: from 29 to 60
  
- Alignment No. 13184
- gi No. 135415
- % Identity 88.9
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1810: from 29 to 55
  
- Alignment No. 13185
- gi No. 135416
- % Identity 72.2
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13186
- gi No. 135417
- % Identity 80.6
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13187
- gi No. 135418
- % Identity 72.2
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13188
- gi No. 135419
- % Identity 72.4
- Alignment Length 29
- Location of Alignment in SEQ ID NO 1810: from 29 to 57
  
- Alignment No. 13189
- gi No. 135420
- % Identity 78.1
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1810: from 29 to 60
  
- Alignment No. 13190
- gi No. 135422
- % Identity 74.3
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1810: from 29 to 63
  
- Alignment No. 13191
- gi No. 135423
- % Identity 71.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1810: from 29 to 63
  
- Alignment No. 13192
- gi No. 135424
- % Identity 75
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13193
- gi No. 135425
- % Identity 77.8
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13194
- gi No. 135426
- % Identity 84.8
- Alignment Length 33
- Location of Alignment in SEQ ID NO 1810: from 29 to 60
  
- Alignment No. 13195
- gi No. 135427
- % Identity 72.2
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13196
- gi No. 135428
- % Identity 82.4
- Alignment Length 34
- Location of Alignment in SEQ ID NO 1810: from 29 to 62
  
- Alignment No. 13197
- gi No. 135430
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13198

- gi No. 135431
- % Identity 77.1
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1810: from 29 to 63
  
- Alignment No. 13199
- gi No. 135431
- % Identity 73.7
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1810: from 29 to 63
  
- Alignment No. 13200
- gi No. 135432
- % Identity 73
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13201
- gi No. 135433
- % Identity 84.4
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1810: from 29 to 60
  
- Alignment No. 13202
- gi No. 135434
- % Identity 84.8
- Alignment Length 33
- Location of Alignment in SEQ ID NO 1810: from 29 to 60
  
- Alignment No. 13203
- gi No. 135435
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13204
- gi No. 135436
- % Identity 82.4
- Alignment Length 34
- Location of Alignment in SEQ ID NO 1810: from 29 to 61
  
- Alignment No. 13205
- gi No. 135437
- % Identity 85.3
- Alignment Length 34
- Location of Alignment in SEQ ID NO 1810: from 29 to 61
  
- Alignment No. 13206
- gi No. 135438
- % Identity 84.4
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1810: from 29 to 60
  
- Alignment No. 13207
- gi No. 135439
- % Identity 76.9
- Alignment Length 39
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13208
- gi No. 135440

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- % Identity 78.4
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13209
- gi No. 135441
- % Identity 80.6
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13210
- gi No. 1362559
- % Identity 75.7
- Alignment Length 39
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13211
- gi No. 1460090
- % Identity 82.4
- Alignment Length 34
- Location of Alignment in SEQ ID NO 1810: from 29 to 62
  
- Alignment No. 13212
- gi No. 1460092
- % Identity 82.4
- Alignment Length 34
- Location of Alignment in SEQ ID NO 1810: from 29 to 62
  
- Alignment No. 13213
- gi No. 1477428
- % Identity 100
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13214
- gi No. 1527170
- % Identity 73
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13215
- gi No. 1527172
- % Identity 73
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13216
- gi No. 1556446
- % Identity 86.5
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13217
- gi No. 1619297
- % Identity 86.5
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13218
- gi No. 1729834
- % Identity 79.3

- Alignment Length 29
- Location of Alignment in SEQ ID NO 1810: from 29 to 57
  
- Alignment No. 13219
- gi No. 1729835
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 1810: from 29 to 57
  
- Alignment No. 13220
- gi No. 1729837
- % Identity 72.2
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13221
- gi No. 1729838
- % Identity 79.4
- Alignment Length 34
- Location of Alignment in SEQ ID NO 1810: from 29 to 62
  
- Alignment No. 13222
- gi No. 1729839
- % Identity 77.8
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13223
- gi No. 1729841
- % Identity 72.2
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13224
- gi No. 1729842
- % Identity 77.8
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13225
- gi No. 173058
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 1810: from 29 to 57
  
- Alignment No. 13226
- gi No. 1854669
- % Identity 77.8
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13227
- gi No. 202223
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13228
- gi No. 202225
- % Identity 70.3
- Alignment Length 37

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- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13229
- gi No. 2088848
- % Identity 77.8
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13230
- gi No. 2098751
- % Identity 75.7
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13231
- gi No. 2098753
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13232
- gi No. 2098757
- % Identity 78.4
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13233
- gi No. 2119263
- % Identity 75
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13234
- gi No. 2119268
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13235
- gi No. 2119269
- % Identity 72.2
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13236
- gi No. 212836
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13237
- gi No. 223280
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13238
- gi No. 223556
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

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- Alignment No. 13239
- gi No. 225587
- % Identity 77.8
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13240
- gi No. 226261
- % Identity 83.3
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13241
- gi No. 2401255
- % Identity 77.8
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13242
- gi No. 2511531
- % Identity 83.8
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13243
- gi No. 2511533
- % Identity 81.3
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1810: from 29 to 60
  
- Alignment No. 13244
- gi No. 2511535
- % Identity 97.2
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13245
- gi No. 2522334
- % Identity 77.1
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 63
  
- Alignment No. 13246
- gi No. 2522336
- % Identity 71.1
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13247
- gi No. 2599500
- % Identity 77.8
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13248
- gi No. 2613143
- % Identity 78.4
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13249
- gi No. 2625154
- % Identity 78.4
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13250
- gi No. 2625156
- % Identity 75.7
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13251
- gi No. 267069
- % Identity 88.9
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13252
- gi No. 267070
- % Identity 88.9
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13253
- gi No. 283503
- % Identity 82.4
- Alignment Length 34
- Location of Alignment in SEQ ID NO 1810: from 29 to 62
  
- Alignment No. 13254
- gi No. 2842514
- % Identity 71.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1810: from 29 to 63
  
- Alignment No. 13255
- gi No. 2843123
- % Identity 72.2
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13256
- gi No. 3024695
- % Identity 72.2
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13257
- gi No. 306451
- % Identity 72.2
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13258
- gi No. 3163946
- % Identity 83.8
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13259



- gi No. 32015
- % Identity 74.3
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1810: from 29 to 63
  
- Alignment No. 13260
- gi No. 320182
- % Identity 72.2
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 63
  
- Alignment No. 13261
- gi No. 320192
- % Identity 78.9
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13262
- gi No. 320960
- % Identity 85.3
- Alignment Length 34
- Location of Alignment in SEQ ID NO 1810: from 29 to 61
  
- Alignment No. 13263
- gi No. 3334365
- % Identity 74.4
- Alignment Length 39
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13264
- gi No. 3334366
- % Identity 85.3
- Alignment Length 34
- Location of Alignment in SEQ ID NO 1810: from 29 to 62
  
- Alignment No. 13265
- gi No. 3334366
- % Identity 76.9
- Alignment Length 39
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13266
- gi No. 3348122
- % Identity 72.2
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13267
- gi No. 3745821
- % Identity 87.5
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1810: from 29 to 52
  
- Alignment No. 13268
- gi No. 3876026
- % Identity 71.9
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1810: from 29 to 60
  
- Alignment No. 13269
- gi No. 3876416

- % Identity 75.7
- Alignment Length 39
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13270
- gi No. 3880320
- % Identity 80
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1810: from 29 to 63
  
- Alignment No. 13271
- gi No. 3915082
- % Identity 81.1
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13272
- gi No. 3915086
- % Identity 75.7
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13273
- gi No. 3915092
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13274
- gi No. 3915094
- % Identity 75.7
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13275
- gi No. 401161
- % Identity 100
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13276
- gi No. 4050007
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13277
- gi No. 4090251
- % Identity 72.7
- Alignment Length 33
- Location of Alignment in SEQ ID NO 1810: from 29 to 61
  
- Alignment No. 13278
- gi No. 4090271
- % Identity 77.1
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1810: from 29 to 63
  
- Alignment No. 13279
- gi No. 4098272
- % Identity 83.8

- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13280
- gi No. 416222
- % Identity 81.1
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13281
- gi No. 4165488
- % Identity 83.8
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13282
- gi No. 4206112
- % Identity 91.9
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13283
- gi No. 421757
- % Identity 81.1
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13284
- gi No. 4416179
- % Identity 84.4
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1810: from 29 to 60
  
- Alignment No. 13285
- gi No. 4583673
- % Identity 81.5
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1810: from 29 to 55
  
- Alignment No. 13286
- gi No. 464840
- % Identity 83.8
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13287
- gi No. 464841
- % Identity 83.3
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13288
- gi No. 464846
- % Identity 100
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13289
- gi No. 464847
- % Identity 81.1
- Alignment Length 37

- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13290
- gi No. 464849
- % Identity 88.9
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13291
- gi No. 4741827
- % Identity 73
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13292
- gi No. 477233
- % Identity 75.7
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13293
- gi No. 477265
- % Identity 77.8
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13294
- gi No. 4929136
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13295
- gi No. 5174477
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13296
- gi No. 5174733
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13297
- gi No. 539933
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13298
- gi No. 542179
- % Identity 81.1
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13299
- gi No. 549051
- % Identity 73
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13300
- gi No. 549052
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13301
- gi No. 55775
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13302
- gi No. 586073
- % Identity 84.4
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1810: from 29 to 60
  
- Alignment No. 13303
- gi No. 586074
- % Identity 84.4
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1810: from 29 to 60
  
- Alignment No. 13304
- gi No. 606648
- % Identity 78.4
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13305
- gi No. 630460
- % Identity 77.1
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1810: from 29 to 63
  
- Alignment No. 13306
- gi No. 630460
- % Identity 73.7
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1810: from 29 to 63
  
- Alignment No. 13307
- gi No. 65165
- % Identity 80.6
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13308
- gi No. 71575
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13309
- gi No. 71577
- % Identity 71.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1810: from 29 to 63

- Alignment No. 13310
- gi No. 730899
- % Identity 84.4
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1810: from 29 to 60
  
- Alignment No. 13311
- gi No. 84169
- % Identity 77.8
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13312
- gi No. 84373
- % Identity 78.1
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1810: from 29 to 60
  
- Alignment No. 13313
- gi No. 90217
- % Identity 75.7
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
  
- Alignment No. 13314
- gi No. 942596
- % Identity 73
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1811
- Ceres seq\_id 1501282
- Location of start within SEQ ID NO 1809: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 284113

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1812
- Ceres seq\_id 1501306

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1813
- Ceres seq\_id 1501307
- Location of start within SEQ ID NO 1812: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1814
- Ceres seq\_id 1501308
- Location of start within SEQ ID NO 1812: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1815
- Ceres seq\_id 1501309
- Location of start within SEQ ID NO 1812: at 146 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13315
- gi No. 3935169
- % Identity 80.9
- Alignment Length 68
- Location of Alignment in SEQ ID NO 1815: from 1 to 68
- Alignment No. 13316
- gi No. 3935171
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 1815: from 1 to 53

Maximum Length Sequence corresponding to clone ID 284115

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1816
- Ceres seq\_id 1501310

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1817
- Ceres seq\_id 1501311
- Location of start within SEQ ID NO 1816: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13317
- gi No. 3894190
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1817: from 69 to 90

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1818
- Ceres seq\_id 1501312
- Location of start within SEQ ID NO 1816: at 16 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13318
- gi No. 3894190
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1818: from 64 to 85

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1819
- Ceres seq\_id 1501313
- Location of start within SEQ ID NO 1816: at 61 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13319

- gi No. 3894190
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1819: from 49 to 70

Maximum Length Sequence corresponding to clone ID 284319

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1820
- Ceres seq\_id 1501318

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1821
- Ceres seq\_id 1501319
- Location of start within SEQ ID NO 1820: at 182 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13320
- gi No. 1743354
- % Identity 75
- Alignment Length 28
- Location of Alignment in SEQ ID NO 1821: from 28 to 55

Maximum Length Sequence corresponding to clone ID 284342

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1822
- Ceres seq\_id 1501324

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1823
- Ceres seq\_id 1501325
- Location of start within SEQ ID NO 1822: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13321
- gi No. 2385410
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1823: from 144 to 179
- Alignment No. 13322
- gi No. 586324
- % Identity 71.8
- Alignment Length 39
- Location of Alignment in SEQ ID NO 1823: from 142 to 179

Maximum Length Sequence corresponding to clone ID 284346

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1824
- Ceres seq\_id 1501326

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1825
- Ceres seq\_id 1501327
- Location of start within SEQ ID NO 1824: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13323
- Initiation factor 2 subunit
- Location within SEQ ID NO 1825: from 92 to 177 aa.



(D) Related Amino Acid Sequences

- Alignment No. 13324
- gi No. 1085819
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1825: from 70 to 80

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1826
- Ceres seq\_id 1501328
- Location of start within SEQ ID NO 1824: at 62 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13325
- Initiation factor 2 subunit
- Location within SEQ ID NO 1826: from 72 to 157 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13326
- gi No. 1085819
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1826: from 50 to 60

Maximum Length Sequence corresponding to clone ID 284539

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1827
- Ceres seq\_id 1501329

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1828
- Ceres seq\_id 1501330
- Location of start within SEQ ID NO 1827: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1829
- Ceres seq\_id 1501331
- Location of start within SEQ ID NO 1827: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13327
- Glycosyl hydrolase family 1
- Location within SEQ ID NO 1829: from 48 to 162 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 284568

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1830
- Ceres seq\_id 1501339

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1831
- Ceres seq\_id 1501340
- Location of start within SEQ ID NO 1830: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13328
- Purine/pyrimidine phosphoribosyl transferases
- Location within SEQ ID NO 1831: from 51 to 135 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1832
- Ceres seq\_id 1501341
- Location of start within SEQ ID NO 1830: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1833
- Ceres seq\_id 1501342
- Location of start within SEQ ID NO 1830: at 73 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13329
- Purine/pyrimidine phosphoribosyl transferases
- Location within SEQ ID NO 1833: from 27 to 111 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 284741

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1834
- Ceres seq\_id 1501345

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1835
- Ceres seq\_id 1501346
- Location of start within SEQ ID NO 1834: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13330
- gi No. 1644232
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1835: from 43 to 53
- Alignment No. 13331
- gi No. 4505323
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1835: from 43 to 53

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1836
- Ceres seq\_id 1501347
- Location of start within SEQ ID NO 1834: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1837
- Ceres seq\_id 1501348
- Location of start within SEQ ID NO 1834: at 80 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 284789

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1838
- Ceres seq\_id 1501364

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1839
- Ceres seq\_id 1501365
- Location of start within SEQ ID NO 1838: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1840
- Ceres seq\_id 1501366
- Location of start within SEQ ID NO 1838: at 131 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13332
- Aldo/keto reductase family
- Location within SEQ ID NO 1840: from 13 to 126 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13333
- gi No. 1935911
- % Identity 90.4
- Alignment Length 52
- Location of Alignment in SEQ ID NO 1840: from 76 to 126

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1841
- Ceres seq\_id 1501367
- Location of start within SEQ ID NO 1838: at 212 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13334
- Aldo/keto reductase family
- Location within SEQ ID NO 1841: from 1 to 99 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13335
- gi No. 1935911
- % Identity 90.4
- Alignment Length 52
- Location of Alignment in SEQ ID NO 1841: from 49 to 99

Maximum Length Sequence corresponding to clone ID 285304

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(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1842
- Ceres seq\_id 1501400

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1843
- Ceres seq\_id 1501401
- Location of start within SEQ ID NO 1842: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1844
- Ceres seq\_id 1501402
- Location of start within SEQ ID NO 1842: at 330 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13336
- gi No. 2997589
- % Identity 100
- Alignment Length 62
- Location of Alignment in SEQ ID NO 1844: from 1 to 61

Maximum Length Sequence corresponding to clone ID 285353

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1845
- Ceres seq\_id 1501416

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1846
- Ceres seq\_id 1501417
- Location of start within SEQ ID NO 1845: at 140 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13337
- Helix-loop-helix DNA-binding domain
- Location within SEQ ID NO 1846: from 65 to 113 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1847
- Ceres seq\_id 1501418
- Location of start within SEQ ID NO 1845: at 143 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13338
- Helix-loop-helix DNA-binding domain
- Location within SEQ ID NO 1847: from 64 to 112 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 285545

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1848
- Ceres seq\_id 1501439

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1849
- Ceres seq\_id 1501440
- Location of start within SEQ ID NO 1848: at 87 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13339
- Pyruvate kinase
- Location within SEQ ID NO 1849: from 25 to 143 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1850
- Ceres seq\_id 1501441
- Location of start within SEQ ID NO 1848: at 231 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13340
- Pyruvate kinase
- Location within SEQ ID NO 1850: from 1 to 95 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1851
- Ceres seq\_id 1501442
- Location of start within SEQ ID NO 1848: at 261 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13341
- Pyruvate kinase
- Location within SEQ ID NO 1851: from 1 to 85 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 285623

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1852
- Ceres seq\_id 1501471

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1853
- Ceres seq\_id 1501472
- Location of start within SEQ ID NO 1852: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13342
- DNA topoisomerase II (N-terminal region)
- Location within SEQ ID NO 1853: from 1 to 117 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 285664

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1854
- Ceres seq\_id 1501485

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1855

- Ceres seq\_id 1501486
- Location of start within SEQ ID NO 1854: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13343
- gi No. 2134209
- % Identity 70.4
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1855: from 64 to 90

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1856
- Ceres seq\_id 1501487
- Location of start within SEQ ID NO 1854: at 88 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 13344
- Aspartate/ornithine carbamoyltransferase
- Location within SEQ ID NO 1856: from 70 to 141 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1857
- Ceres seq\_id 1501488
- Location of start within SEQ ID NO 1854: at 91 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 13345
- Aspartate/ornithine carbamoyltransferase
- Location within SEQ ID NO 1857: from 69 to 140 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 285671

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1858
- Ceres seq\_id 1501489

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1859
- Ceres seq\_id 1501490
- Location of start within SEQ ID NO 1858: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13346
- gi No. 2507155
- % Identity 81.8
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1859: from 1 to 11
  
- Alignment No. 13347
- gi No. 3122386
- % Identity 85.5
- Alignment Length 145
- Location of Alignment in SEQ ID NO 1859: from 48 to 191

- Alignment No. 13348
- gi No. 3122387
- % Identity 84.1
- Alignment Length 145
- Location of Alignment in SEQ ID NO 1859: from 48 to 191
  
- Alignment No. 13349
- gi No. 439289
- % Identity 81.8
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1859: from 1 to 11
  
- Alignment No. 13350
- gi No. 465445
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1859: from 5 to 15
  
- Alignment No. 13351
- gi No. 871535
- % Identity 81.8
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1859: from 1 to 11

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1860
- Ceres seq\_id 1501491
- Location of start within SEQ ID NO 1858: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 285805

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1861
- Ceres seq\_id 1501515

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1862
- Ceres seq\_id 1501516
- Location of start within SEQ ID NO 1861: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13352
- Elongation factor 1 (beta/delta chain)
- Location within SEQ ID NO 1862: from 126 to 251 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13353
- gi No. 232031
- % Identity 85.2
- Alignment Length 225
- Location of Alignment in SEQ ID NO 1862: from 33 to 251
  
- Alignment No. 13354
- gi No. 232033
- % Identity 82.6
- Alignment Length 223
- Location of Alignment in SEQ ID NO 1862: from 33 to 251

- Alignment No. 13355
- gi No. 461073
- % Identity 86.7
- Alignment Length 30
- Location of Alignment in SEQ ID NO 1862: from 180 to 209

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1863
- Ceres seq\_id 1501517
- Location of start within SEQ ID NO 1861: at 99 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13356
- Elongation factor 1 (beta/delta chain)
- Location within SEQ ID NO 1863: from 94 to 219 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13357
- gi No. 232031
- % Identity 85.2
- Alignment Length 225
- Location of Alignment in SEQ ID NO 1863: from 1 to 219
  
- Alignment No. 13358
- gi No. 232033
- % Identity 82.6
- Alignment Length 223
- Location of Alignment in SEQ ID NO 1863: from 1 to 219
  
- Alignment No. 13359
- gi No. 461073
- % Identity 86.7
- Alignment Length 30
- Location of Alignment in SEQ ID NO 1863: from 148 to 177

Maximum Length Sequence corresponding to clone ID 285925

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1864
- Ceres seq\_id 1501543

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1865
- Ceres seq\_id 1501544
- Location of start within SEQ ID NO 1864: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13360
- gi No. 1155261
- % Identity 90.1
- Alignment Length 151
- Location of Alignment in SEQ ID NO 1865: from 44 to 193
  
- Alignment No. 13361
- gi No. 135054
- % Identity 74.1
- Alignment Length 147
- Location of Alignment in SEQ ID NO 1865: from 48 to 193